E36050 Signal reco AP003133 Staphyloc AP004826 Staphyloc AF004826 Staphyloc AF004826 Staphyloc AF0050 Staphyloc AF417016 Sequence AX417046 Sequence AX417046 Sequence D14356 Bacillus su

AX417046 AX416333

Description

SUMMARIES

AE006331 Lactococc AP001515 Bacillus AP001519 Clostridi AE010040 Streptococc U88582 Streptococc ARA981886 Sequence ARA95303 Sequence E35383 Novel ffh.

AR081886 AR195303

BD003726 AE007428

AE008489

AX194269

E35383

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Signal recognition particle polypeptide and polynucleotide.
E36050.
E36050.1 GI:13022452
JP 1999235183-A/1.
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Michael, T.B.
Signal recognition particle polypeptide and polynucleotide
Patent: JP 1999235183-A 1 31-AUG-1999;
SMITHKLINE BEECHAM CORP
                                                                                                                                  Query
Match Length DB
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E36050
LOCUS
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SOURCE
ORGANISM
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AUTHORS
TITLE
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                                                                                                                                                        No.
                                                                                                                                                                         ; Search time 3647 Seconds
(without alignments)
10916.545 Million cell updates/sec
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                   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                            February 24, 2003, 20:06:00
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                                                                                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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9D_sr: *
9D_vi: *
em_ba: *
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AX194269 Sequence
AE0003428 Polynucle
AE0003489 Streptoco
AX194043 Serpetoco
AX194043 Serpetoco
AX194043 Serpetoco
AX434343 Sequence
AE000568 Cireptoco
AX43343 Sequence
AE010684 Clostridi
AE010684 Elsobacte
U33696 Haemophilus
AE011144 Buchnera
AE013692 Zersinia
AX013692 Zersinia
AX013692 Zersinia
AX114156 Persinia
AX013104 Thermoana
AE001119 Buchnera
AE001119 Buchnera
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AE014153 AX194043

ALIGNMENTS

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BCT 02-JUL-2002
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Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
Sekimizu,K., Hirakawa,H., Kuhra,S., Goto,S., Yabizaki,J.,
Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus subsp. aureus N315 (sub_species:aureus N315,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1261 AACGATATGAAGAAATGATGAAAACAATTCACTGGTGGCGGTAAAAGGTAAAAAAGGTAAA 1320
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                                                                            1081 AAAGGGCTAGATAAGCTTAATATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1141 CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACACATTGAATGTATCACGTAAAAAG
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                             601 GCATIGAIGAACGAATTAAAAGAAGIAAAAGAAATIGCIAAACCAAACGAAATTAIGITA
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   GCATTGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAACCAAACGAAATTATGTTA
                                                              GTTGTCGATTCAATGACGGGTCAAGATGCTGTCAATGTTGCAGAATCTTTTGACGATCAA
                                                                                                                          CITGATGTCACAGGTGTTACCTTAACTAAATTAGATGGTGATACACGTGGTGGTGCTGCCAGCT
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Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                       A61K39/085,
A61K39/395,A61K39/395,A61K48/00,C07K14/31,C07K16/12,C12N1/15,
                                                                                   CL2N15/09, A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/00,
                                                                                                                       A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/70, A61K35/76
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                                                          60/057890,05-MAR-1998 US
                                                                                                                                                                                                                                                                                                              ce 1. 1368
/organism='Unidentified'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1368; DB 6;
Pred. No. 5.3e-220;
; Mismatches 0;
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    11. 1368
/organism="unidentified"

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186 c 288 q
                                            03-SEP-1998 JP 1998289963
03-SEP-1997 US 60/0578
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Strandedness: Single;
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              JP 1999235183-A/1
                                                                            AEL TERENCE BLACK
                                                                                                                                                                                                                                                                                  Topology: Linear;
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PPPVKKVANKYDLEPVYQPEKLSGSEELEQLLQLDVDLIVTAARGQLLPESLLALPKLG
AINVHASLLPKYRGGAPTHQAIDGEGETGTTMYNVKKLDAGNIISQQAIKIEENDN
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EAVAIKDMQLAGKKRMLAANYLSGAQNTLVGKKLI"
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CVCALVPEKSVVIANVGDSRAYVINSRQIEQITSDHSFVNHLVLFGQITPEEAFFPQ
RNIITKVMGTDKRVSPDLFIKRLNFYDYLLLNSDGIFDYVKDNEIKRLLVKBGTIEDH
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Prekeetlekeferbynssolshonivsmidvdeeddcyvlomstiegptlseviesh
Gplsydtalnethotikhandnetvhromidskontlidsnktalfergiakalse
Tsltotitertotivgyrfspegakgratdectiltsississer
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TKPYDKTYDKILVDAPCSGLGVWRHKPEIKYTQSKQHIESLVELVLEUVKNNVVKI
GGEIIYSTCTIEQLENENVIYTFLKNNKNFEFEPFQHPITGELVKTLQIMPQDFNSDG
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DFADEDIQINPAVSLHAAKDEVRSRLMPINRAYNVEKLIEAIQYYQEKTNRRVTFEYG
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ADPKKRMALEYSWPKWIIDHWATHYGLBETETILQSFLETTSTTVRANLTRASLDDII
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QIFBWLYQKRVDSIDEMTNLSKDLRQLLKDNFTVTTLTTVVKQESKDGTIKFLFELQD
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                                                                                                                                                                                                                                                                                           hypothetical protein, similar to RNA-binding Sun protein"
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/gene="SAL062"
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/gene="SAL062"
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4543. .5637
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/gene="SA1060"
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⟨translation="movnkvlyillalfigsfg]Hkfyacknmggllhlifcwtg]PH
IIAIISAVITVFKPADEgGNVTL"

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LVHMDFLNASSDFGNAHFVVLSKIIKĒYESNYĒTASDDSLK"
complement(1318. .1521)
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hypothetical protein, similar to polypeptide deformylase"
/codon_start=1
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Aoki,K., Oguchi,A., Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K.
and Kikuchi,H.
Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                      Submitted (30-JAN-2001) Akio Oguchi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishinara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:oguchi@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8423, Fax:81-3-3481-8424) On Jun 12, 2001 this sequence version replaced gi:13701012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Staphylococcus aureus subsp. aureus N315"
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product="methionyl-tRNA formyltransferase"
/protein_id="Bab42311.1"
/db_xref="G1:13701016"
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                                                     Lancet 357 (9264), 1225-1240 (2001)
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/gene="SA1058"
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IKHLDKKAGVVINPGTPISQIEPILDIVDYVLVWTYNPGFGGQSFIDQCVEKIAGLNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26606 CCTACTGTTGTTATGATGGTTGGTTTACAAGGTGCTGGTAAAAACAACAACTGCAGGTAAA 26665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26306 ATGGCATTTGAAGGCTTATCAGAACGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAG 26365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26666 TTAGCATTATTGATGCGTAAAAATACAACAAAAACCTATGTTAGTTGCAGCAGATATT 26725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKMERQLNFDIEVDGGVNTDTAKVCVENGATMLVTGSFFFKQEDYKKVTQALKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTAGGTICCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATAGTTCAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTAGCATTATTGATGCGTAAAAATACAACAAAAACCTATGTTAGTTGCAGCAGATATT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGCTGACGTAAACTTTAAAGTGGTAAAAGAATTTATTAAAACAGTATCAGAACGCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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ribulose-5-phosphate 3-epimerase homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1368; DB 1; 100.0%; Pred. No. 1.4e-220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                     TLQLFNEISNRKVRY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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BCT 07-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                           27085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27146 GAIGGITIAGAGCIAITCCAICCIGAACGIAIGGCAICACGIAITIIAGGIAIGGGIGAI 27205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27266 GAGAAAAAGATGCGTGAGCTTTACTTTAGATGATTTTTAGAACAACATGATGA 27325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27566 AACGATATGAAGAAAATGATGAAACAATTCACTGGTGGCGGTAAAAGGTAAAAAGGTAAAA 27625
                                             26845
                                                                                                                                                                                                                         GCATTGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAACCAAACGAAATTATGTTA 26965
                                                                                                                                                                                                                                                                                                                   GITGICGAIICAAIGACGGGICAAGAIGCIGICAAIGIIGCAGAAICIIITGACGAICAA 27025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27206 GIGITAAGITTAAITGAAAAGCGCAACAAGAIGIGGAICAAGAAAAAGCAAAAGATITA 27265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGAAAAAGAIGCGIGAGICAICGIIITACIIITAGAIGAIITIITIAGAACAACIIGAICAG 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGAAAAATCTAGGACCACTGGATGATATTATGAAAATGATTCCAGGTATGAATAAAATG 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTATTGCTAAAGGGTCTGGTCGTTCATTACAAGAAGTCAATCGTTTGATGAAACAATTT 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACGATATGAAGAAATGATGAAACAATTCACTGGTGGCGGTAAAGGTAAAAGGTAAA 1320
                                                                                                                                                                                                                                                                                                                                                                780
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTATCTATTCGTTCGGTGACACAAACCAATTAAATTTGTTGGTATGAGTGAAAGTTA 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27446 CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACACTTGAATGTATCACGTAAAAAG
                          GATGGTTTAGAGCTATTCCATCCTGAACGTATGGCATCACGTATTTAGGTATGGGTGAT
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                                                                                                                                                                                                                                                                         GTTGTCGATTCAATGACGGGTCAAGATGCTGTCAATGTTGCAGAATCTTTGACGATCAA
                                                                                                                                                                                                                                                                                                                                                              CTTGATGTCACAGGTGTTACCTTAACTAAATTAGATGGTGATACACGTGGTGGTGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27626 CGCAATCAAATGCAAAATATGTTAAAAGGTATGAATTTACCGTTTTAA 27673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1321 CGCAATCAAATGCAAAATATGTTAAAAGGTATGAATTTACCGTTTTAA 1368
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MRIERVDDTTVKLFITYSDIEARGFSREDLWTNRKRGEEFFWSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKAFLVEFQEKYESFYNSDKLDDILDQGRDKAHKVSFKTVKKMEKAMGLGRKR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3894. .4883)
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5177. EE7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SAV0998"
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5943. . 6667
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6783. .7769
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VVAEFCDKVLVMYAGQIVEFGGIKEILHNPKHPYTQKLLSTIPKLKEGQKRLETIEGI
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                        Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I., Cui,L., Oyuchi,A., Aoki,K., Naqai,Y., Lian,J., Ito,T., Kanamori,M., Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A., Kanamori,M. Mizutani-Ui,Y., Takahashi,M.K., Sawano,T., Inoue,R., Kaito,C., Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J., Kanenisa,M., Yamashita,A., Sahma,K., Furuya,K., Yoshino,C., Shiba,T., Hattori,M., Ogaswara,N., Haysshi,H. and Hiramatsu,K. Whole genome sequencing of meticillin-resistant Staphylococus
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        Arganism="Staphylococcus aureus subsp. aureus Mu50" / strain="Mu50"
    /strain="Mu50"

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                                                                                               AAAGAAGAACATTTAGACTTTGTAATCATTGATACAGCAGGTCGATTACACATCGATGAA
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   TTAGCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGCAGCAGATATT
                                         TTAGCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGCAGCAGATATT
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                                                                                             HTFNLEKKQIMMFQQIQYLGGHKYVAEKRNAKIIELFNEAPCDYHAVYKLSKFAINQY
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Pred. No. 1.3e-220;
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COMplement (1417. .1695)
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hypothetical protein, similar to polypeptide deformylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-MAR-2002) Akio Oguchi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:oguchi@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8423, Fax:81-3-3481-8424)

    .295350
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/strain="MW2"

                                                                                                                                                                                                                Baba,T., Takeuchi,F., Kuroda,M., Yuzawa,H., Aoki,K., Oguchi
Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Cui,L.,
Yamamoto,K. and Hiramatsu,K.
Genome and Virulence determinants of high virulence
community-acquired MRSA
Lancet 359 (9320), 1819-1827 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 295350)
Aok1, K., Oguch1, A., Nagai, Y., Asano, K., Iwama, N., Baba, T.,
Kuroda, M., Hiramatsu, K. and Kikuchi, H.
Direct Submission
                                                                                                         Staphylococcus aureus subsp. aureus MW2 (strain:MW2) DNA. Staphylococcus aureus subsp. aureus MW2
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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FEFVQUININGYTHGVPERRKNELKRPPVSNIDTLYIVMSAYEPNSTQLLDRFLVIAHS
YQLNARVLVYKDKTPIENGFERLELKIYENICYEFFTGNDDRKKYTVBANGAGLI
VLGGQSGVGKSFFLHHYRPELMLETNDISKSLNRGKHTRHVELFERQNGYIADTPG
SALDFDHIDKDEIKDYFLELNRYGETCKFRNCNHIKEPNCWKHQLEIGNIAQPRIDH
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IFNKNNLKLGKISRSYSDKYPENEIIKTTPNTGERVERGDSVDVVISKGPEKVKMPNV
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STISFVVSKGKKSDSSDVKTTTESVDVPYTGKNDKSQKVKYIIKDKDNDGSTEKGSFD
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SIGLIDAVRKGTLPIDHUMLAIRENEEKTYSRRAEAGADMISIHVESTPHIHRALOM
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IKMERQLNFDIEVDGGVNTDTAKVCVENGATMLVTGSFFFKQEDYKKYTQALKG
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/protein_id="BAB94970.1"
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/protein_id="BAB94969
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/note="ORFID:MW1106"
/codon_start=1
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/gene="MW1104"
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/orderia 2058: 0.000.001 to 0.349.980-seq 4032: 0.300.001 to 0.649.980-seq 4032: 0.300.001 to 0.949.980-seq 4035: 1.200.001 to 1.349.980-seq 4035: 1.200.001 to 1.849.980-seq 4035: 1.200.001 to 2.449.980-seq 4039: 2.400.001 to 2.449.980-seq 4039: 2.400.001 to 2.449.980-seq 4040: 2.400.001 to 2.449.980-seq 4040: 3.000.001 to 3.011.208"

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                             Db 189184 GCTGAAATGAAAAAAATGATGAAGCAAATGACTGGTGGGGGGAAAAGGTAAGAAGGTAAA 189243
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Patent: WO 0228891-A 4037 11-APR-2002;
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4037 from Patent W00228891.
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Db 129021 TTTTCTCTAGGCGATCAAGTAAGCCCAGTAGAAATCGCGAAACAAGCTATCGCTAAAGCA 128962
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                                    GCATTGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAAACCAAACGAAATTATGTTA
                                                                                         Db 128901 ACTCTGATGGACGAATTAAAACAAGTGAAAGAAATCGCTACGCCAACTGAAATTTTACTT
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Listeria monocytogenes ATCC 19115
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Patent: WO 0228891-A 3324 11-APR-2002;
Pasteur Institut (FR)
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Sequence 3324 from Patent W00228891.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTGTCGATTCAATGACGGGTCAAGATGCTGTCAATGTTGCAGAATCTTTTGACGATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCGATTCGTTCCGTCACTGGCAAAACTAAAATTATTGTCGCGACTGGTGAAAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                               Length 2256;
                                                                               Indels
                                               Score 697.6; DB 6;
Pred. No. 1.2e-107;
); Mismatches 389;
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 832
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 420
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                                               51.0%;
70.5%;
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                                                                               Conservative
471
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2157. .2429
/gene="rpsp"
/codon_start=1
                                                                                                                                                                                                                                   /gene="rpsp"
2157. .2429
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1 (bases 1 to 2739)
Honda,K., Nakamura,K., Nishiguchi,M. and Yamane,K.
Cloning and characterization of a Bacillus subtilis gene encoding a homoLog of the 54-kilodalton subunit of mammalian signal recognition particle and Escherichia coli Ffh
J. Bacteriol. 175 (15), 4885-4894 (1993)
                                                                                                                                                                                                                                                                                                                                                                             D14356 Bacillus subtilis orfl, ffh, rpsP genes for ORFl, Ffh and 30S ribosomal protein S16, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSLEKTTRMNYLFDFYQSLLISRQKSYMSLYYLDDFSLGEBAEE
FEVSRQAYYDNIKRTEAMLEQYEEKLLLIKKFQERKEMFNKLKELASGSKEEEEITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-FEB-1993) Kunio Yamane, Inst. Biological Sciences, Tsukuba University; Tsukuba, Ibaraki 305, Japan (Tel:0298-53-6419,
                                         1021 GTGAAAATCTAGGACCACTGGATGATATTATGAAAATGATTCCAGGTATGAATAAATG 1080
                                                                                                 1081 AAAGGGCTAGATAAGCTTAATATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATC 1140
                                                                                                                                                                                                                  1201 CGTATIGCTAAAGGGICTGGTCGTTCATTACAAGAAGTCAATCGTTTGATGAAACAATTT 1260
                                                                                                                                                                                                                                                                            406 GGTGBABATGBABABABATGBAGGBABATGBACTGGTGGCGGCBABAGGGCBABABGGCBABA 347
1141 CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACACATTGAATGTATCACGTAAAAAG
                                                                      protein S16; ffh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bacillus subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpsP; orf1; 30S ribosomal protein S
Bacillus subtilis (strain:168) DNA
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAA22221.1"
/db_xref="GI:2424968"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315. .320
/evidence=experimental
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'product="ORF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="orf1"
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/gene="orf1"
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/gene="ffh"
711. .2051
/gene="ffh"
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D14356.1
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TITLE
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REFERENCE
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/translation="MAVXIRLKRMGAKKSPFYRIVVADSRSPRDGRFIEFVGTYNPVA
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527 c 648 g 677 t
                                                                                                             VIMMVGLQGAGKTTTSGKLANLLRKKHNRKPNIVAÅDIYRPAAIKQLETLGKQLDNEV
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FLVVDSWTGQDAVNVAKSFNEQLGLTGVVLTKLDGDTRGGAALSIRAVTNTPIKFAGL
                                                                                                                                                                                                GEKLDALEPFHPERMASRILGMGDVLTLIEKAQASVDEDKAKELEQKMRTMSFTLDDF
LEQLGQVRNMGPLDELLQMMPGAGKMKCLKNIQVDEKQLNHVEAIIKSMTVLEKEGPD
IINASRRKRIAKGSGTSVQEVNRLLKQPDEMKKAMKQMTNMSKGKRKGFKLPFM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1011 CCGACTGTTATTATGATGGTCGGTCTCCAAGGTGCCGGTAAAACGACAACAAGCGGTAAG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1131 TACCGCCCCAGCCGCAATTAAGCAGCTGGAACACTCGGCAAACAGCTTGATATGCCTGTT 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGAATTAACGAAGTTGATGGGTGGAGAAATACATCGATTAATATGTCAAATAAACCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTACTGTTGTTATGATGGTTGGTTTACAAGGTGCTGGTAAAACAACAACTGCAGGTAAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 TTAGCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGCAGCAGATATT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATCGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACAGTGAAGGAGATCAAGTAAAGCCACAAAATTGTAACTAATGCATTAAAACATGCT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 AAAGAAGAACATTTAGACTTTGTAATCATTGATACAGCAGGTCGATTACACATCGATGAA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GAGGCTGACGTAAACTTTAAAGTGGTAAAAGAATTTATTAAAACAGTATCAGAACGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATAGTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGCATTTGAAGGCTTATCAGAAGGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2739;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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Pred. No. 3.9e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 432;
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/db_xref="G1:2309080"
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S Kunst, F., Ogasavara, M., Moszer, I., Albertini, A.M., Alloni, G.,
Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S.,
Borriss, R., Bourieler, L., Brans, A., Brann, M., Brignell, S.C.,
Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V.,
Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J.,
Danalel, R.A., Denizoot, F., Devine, K.M., Dustenfoft, A., Enfich, S.D.,
Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E.,
Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A.,
Galleron, N., Ghlm, S.Y., Glaser, P., Goffeu, A., Golightly, E.J.,
Grandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R.,
Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F.,
Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCT 26-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BSUB0009 208780 bp DNA linear BCT 26-NOV-1998 Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACTGATGGATGAACTGACCAACGTCAAAGAAATCGCGAATCCGGAAGAAATTTTCCTG 1370
                                                                                                                                                       GIGAAAAATCTAGGACCACTGGATGATATTATGAAAATGATTCCCAGGTATGAATAAATG 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1081 AAAGGGCTAGATAAGCTTAATATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATC 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1141 CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACACTTGAATGTATCACGTAAAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1851 AAATCAATGACTGTTCTTGAAAAGAACAGCGGGATATTATCAATGCCAGCGGGGGAAG 1910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTATTGCTAAAGGGTCTGGTCGTTCATTACAAGAAGTCAATCGTTTGATGAAACAATTT 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGCGTTAGAGCCGTTCCATCCTGAACGCATGGCATCAAGGATTCTCGGCATGGGCGAC 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAAAAAGATGCGTGAGTCATCGTTTACTTTAGATGATTTTTTTAGAACAACTTGATCAG 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1671 GAACAAAAARIGAGAACGATGAGCTTCACATTGGACGATTTTCTGGAGCAGCTCGGGCAA 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1791 AAGGGCCTGAAAAACATCCAAGTTGATGAAAAACAGCTGAATCATGTGGAAGCAATCATC 1850
                                                                                                                    GTTGTCGATTCAATGACGGGTCAAGATGCTGTCAATGTTGCAGAATCTTTTGACGATCAA 720
                                                                                                                                                                                                                                            CITGATGTCACAGGTGTTACCTTAACTAAATTAGATGGTGATACACGTGGTGGTGCAGCT 780
                                                                                                                                                                                                                                                                                                                                                                 TTATCTATTCGTTCGGTGACACAAAACCAATTAAATTTGTTGGTATGAGTGAAAGTTA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGGTTTAGAGCTATTCCATCCTGAACGTATGGCATCACGTATTTTAGGTATGGGTGAT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTTAAGTTTAATTGAAAAAGCGCAACAAGATGTGGGATCAAGAAAAAAGATTTA 960
GCATTGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAACCAAACGAAATTATGTTA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1261 AACGATATGAAGAAAATGATGAAACAATTCACTGGTGGCGGTAAAAGGTAAAAA 1314
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Z99112.1 GI:2633902
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REFERENCE AUTHORS TITLE JOURNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TIAGGTICCGAIGTAAIGCAAICAITAACACCAGGGCAACAAGIIAITAAAAIAGIICAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAGCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGCAGCAGATATT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGAATTAACGAAGTTGATGGGTGGAGAAAATACATCGATTAATATGTCAAATAAACCA 300
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                                                                                                                                         'note="similar to acetylornithine deacetylase"
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Pred. No. 1.3e-95;
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terminator
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general bluds to the conserved sequence in the pyr operon mrna and distorts the antiferminator, permitting terminator hairply formation and promoting transcription termination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="UNKNOWN PROTEIN"
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/db_xref="G1:12724612"
/db_xref="G1:12724612"
/translation="MQDF1QYYSAFERIADFSDQQKIILLGLICGLLIAIFLYPLLR
ILVPLLHEFGHALAAKITFGKYYRIHINHDSSGLTQTSGGGRSFFYLLMGYPMPLFG
CLFSWFLIINHPEFILISLLIVSLSVLIVVKNWYGFLICLLGILITGALLYFGQIQIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MARKETIDEITMKRAITRITYEIIERNKELDKLVLIGIKTRGVY
LAKRIQERLQQLEGLEIPRGELDTRPREDDKQAQEDTTEIDIDITGKDVILVDDVLYT
GRTIRAAIDGIVKLGRPARVQLAVLVDRGHRELPIRADYVGKNIPTGRDEEIIVQMSE
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LFLIITTFKTLFSK"
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SLVSQQLKLLKNARILINEKIGKTVTYSIIDRHILHLLKDVAEHLDEQBGGNHEP"
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General. BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
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                                                                             Genetique Microbienne, Domaine
2 (bases 1 to 11023)
Bolotin,A., Wincker,P., Mauger,S., Jaillon,O., Malarme,K., Weissenbach,J., Ehrlich,S.D. and Sorokin,A.
Direct Submission
Submitted (09-JAN-2001) INRA, Genetique Microbienne, Domai Vilvert, Jouy en Josas 78352, France
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                                                                                                                                                       /organism="Lactococcus lactis subsp. lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="pyrimidine operon regulator"
/protein_id="AAK05702.1"
/db_xref="GI:12724611"
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/protein_id="AAK05704.1"
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/protein_id="AAK05705.1"
/db_xref="G1:12724614"
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complement(860. .1558)
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                                                                                                                                                                       /strain="IL1403"
/sub_species="lactis"
                                                                                                                                                                                                             /db_xref="taxon:1360"
complement(78. .599)
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                                                                                                                   Location/Qualifiers
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/gene="rarA"
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/gene="rarA"
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/gene="yqeI"
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The complete genome sequence of the lactic acid bacterium Genome Res. 11 (5), 731-753 (2001)
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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ITGSFPULDEAVPRFPRDPOPVBATGALAFATVANGFSMALLARGSRUESLINLIA
ALEDVALGWLGWLGYLLYSTVHFVKWYWDPLLSILIALFILSKAIPKFWGTLRILLESVP
EDIDYKNLLRALEQLPEVLAVTQLIIWSIDGEQNAAMIHIVIPENQDFSDAKIAVRKL
                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAK05706.1"
/db_xref="GI:12724615"
/translation="MIEELGLKVKKASKEVAKLSTADKNVFLQNLADSLIENTDRIIS
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ETGVGNCTIFVDESADLEMATKIVINAKTQRPSVCNAAESLVVHAKIADEFLPKLENE
INKVHEIEFRADERALKVLSAGIPATDDDFGTEFLDYILSVKTVDNLDEAIEHINTS
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LINNKGFYTLYTGSALQYGLNYTGTOKREPKGTAPQQALASTGQYELMSYTYQMFRRYS
QKVSQLLLTRDYDFPTSREARBNALNALLGILF IP IINNNDALAYDEMDHQYFRGDN
DKLGALVKANNADLLIMLSDIDGLFDKNPSIYDDAKIFNEHEITDELRQMAGGAGG
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VSETIGASTAALIQGGLNFSEIQKLYNHAAVPKGATYDIHEKSLEEPTPYKL
BNOYITSLINDE TRWVFSKIEKGDWSVREALLAAVIDLXNIDKHYARKETLIFSFNER
GITAPPKVWGGVDDSVREMIKKVIVIKTDKTALNALDERDLATEIEDKIFKEER
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SAKAMTEAIAKESGLEVSKPKRVKRQYDWEKVTSEGVVVLPTGMLHLNELTALFNVLP
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QADFWIDLHRFNKKIYIRYFAMRDEETGEYLGCLEVSQDITSIQNLVGEKRLDGHEKT
'translation="MSLKNKQIKSEHDHNHLDKLVSONVTIVFALNLFFAILEFIFGY
                                                                                                                                                                                                                                                                 /hote="EVIDENCE BY HOMOLOGY BIO01.05 Glutamate family.
SECOND STEP IN PROLINE BIOSYNTHESIS PATHWAY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="EVIDENCE BY HOMOLOGY BIO01.05 Glutamate family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFGTGGMTSKLAAAQILFENGQEMVLTNGERIREIKEIIEGREIGTYFHQKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="EVIDENCE BY HOMOLOGY BIO15.02 HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                          /product="gamma-glutamyl phosphate reductase (EC
[.2.1.41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="YqfB"
note="EVIDENCE BY GENEMARK BIO16.01 Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="glutamate 5-kinase (EC 2.7.2.11)"
/protein_id="AAK05707.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIRST STEP IN PROLINE BIOSYNTHESIS PATHWAY
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/db_xref="GI:12724617"
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                                                                                                                         LESEKVCRSAIELDETTDEHKKHVQYEI"
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/gene="proB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5141. .6613)
/gene="YqfA"
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                                                                                                                                                                                                                   complement(2940. .4181)
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                                                                                                                                               complement(2940. .4181)
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/transl_table=11
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                                                                                                                                                                                          /note="L0116"
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/translation="MNSELFEKGGLKDTMPTVFGY1G1G1AFGMIGHSEGFSVWVILL
LSL1VTAGSAQFIMVSMLATHSPIMSTVLSVFLVNSRIILMASMTAASYFKNESLIKNI
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VPVVIMSALWISNLFIQHLGHLPSVNWNNLLASIPTVLAAIITKNLLVIVLVGVFSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="WVIDENCE BY HOMOLOGY BIO13.02 TRANSPORT AND BINDING PROTEINS. Amino acids, peptides and amines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TTAGGTTCCGATGTAATGCAATCATTAACACCCAGGGCAACAAGTTATTAAAATAGTTCAA 240
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0
                                                                                                                                                                                                complement(6979. .7305)
/gene="YqfC"
/note="EVIDENCE BY GENEMARK BIO16.01 Unknown"
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Pred. No. 6.3e-86;
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/product="amino acid permease"
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/protein_id="AAK05709.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7292. .7999)
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                                /db_xref="GI:12724618"
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/db_xref="G1:12724620"
                                                                                                                                                                                                                                                                                                                                          /product="UNKNOWN
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/note="L54719"
                                                                                                                                             /gene="yqfC"
/note="L54406"
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9 (sites)
Nakasone,K., Masui,N., Takaki,Y., Sasaki,R., Maeno,G., Sakiyama,T.,
Hirama,C., Fuji,F. and Takami,H.
Characterization and comparative study of the rrn operons of
alkaliphilic Bacillus halodurans C-125
Extremophiles 4 (4), 209-214 (2000)
                                                                                                                                                                        Takami, H., Nakasone, K., Ogasawara, N., Hirama, C., Nakamura, Y., Masui, N., Fuji, P., Takaki, Y., Inoue, A. and Horikoshi, K. Sequencing of three lambda clones from the genome of alkaliphilic Bacillus sp. strain C-125
Extremophiles 3 (1), 29-34 (1999)
                                                                                                                                                                                                                                                                                                                                                                       Horikoshi,K. Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125 Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28 (21), 4317-4331 (2000)
                                              2 (sites)
Takami, H. and Horikoshi, K.
Reidentification of facultatively alkaliphilic Bacillus sp. C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome analysis of facultatively alkalihilic Bacillus halodurans
C-125
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Takami, H. and Horikoshi, K.
Analysis of the genome of an alkaliphilic Bacillus strain from .
Industrial point of view
Extremophiles 4 (2), 99-108 (2000)
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Submitted (22-M2R-2000) Hideto Takami, Japan Marine Science and
Technology Center, Deep-sea Microorganisms Research Group; 2-15
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
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Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and
Horikoshi,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 (sites)
Takani, H., Masui, N., Nakasone, K. and Horikoshi, K.
Replication origin region of the chromosome of alkaliphilic
Bacillus halodurans C-125
Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)
99356711
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Takaki,Y., Nakasone,K., Sakiyama,T., Maeno,G.,
Sasaki,R., Hirama,C., Fuji,F. and Masui,N.
Genetic analysis of the chromosome of alkaliphilic Bacillus
halodurans C-125
                                                                                                                                                                                                                                                                                                                                  4 (sites)
Takami, H., Takaki, Y., Nakasone, K., Hirama, C., Inoue, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extremophiles in deep-sea environments, 249-284 (1999)
                                                                                                          to Bacillus halodurans
Biosci. Biotechnol. Biochem. 63, 943-945 (1999)
3 (sites)
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Takami, H. and Takaki, Y.
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Takami,H.
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Takami, H., Nakasone, K., Hirama, C., Takaki, Y., Masui, N., Fuji, F.,
Nakamira, Y. and Inoue, A.
An improved physical and genetic map of the genome of alkaliphilic
Bacillus sp. C-125
Extremophiles 3 (1), 21-28 (1999)
                                         10474 INIGARGAAGTGCTGAAAAACCAGTTAATATTGTTCGTAATGGTCTTTTAAAAGCT 10415
                                                                                                                                                                                                      10354 ACTTTAATGAACGAATTGCAAGAGATTAAAGCACTTGCTGAAACCAACTGAAATTTGCTT 10295
                                                                                                                                                                                                                                                                                         10234 TIGGACATTACAGGIGIGAITAICACTAAACTIGAFGGIGAFACACGGGGGGGGGGGG 10175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10114 ACAGACCTIGAAGITITCTAICCIGAATGAGITCACGAAITCTIGGAAIGGGIGAI 10055
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                                                                                                                                                                            601 GCATTGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAACCAAACGAAATTATGTTA 660
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                                                                                                              TACAGTGAAGGAGATCAAGTAAAGCCACAACAAATTGTAACTAATGCATTAAAACATGCT
                                                                                                                                                                                                                                                                  GTTGTCGAJTCAATGACGGGTCAAGATGCTGTCAATGTTGCAGAATCTTTTGACGATCAA
                                                                                                                                                                                                                                                                                                                                                     721 CTTGATGTCACAGGTGTTACCTTAAATTAGATGGTGATACACGTGGTGGTGCTGCAGCT
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                                                                                     541 AAAGAAGAACATTTAGACTTTGTAATCATTGATACAGCAGGTCGATTACACATGGAA
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4864. .5193
                                                                          FAIFVGPNIPFDQKFQVALQQAELFHEKILKKHPQFSFIERWDDLLFLDADQIGAILT
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/product=1heat shock protein class I (low molecular weight) = |
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Pred. No. 8.8e-86;
); Mismatches 455;
                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB05991.1"
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/gene="BH2273"
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STTEG"
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QTIEQLINEQLLQQAATEKEIEVSEEEIDEELAFIVAQFSSEERLMEALEEGGSSMDE
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VLSGLHGTVGVYEPLGEADVAKAEAAIETFGIJHHLTDERPLILSQGERKRAFLARAWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKNHIHTIMEDWKLSGTALMKKGEDIPFIASLGFANRAERIPNE
HHTRFGIASGCKLFTAIAICQLVEAGKLSFDTPLSDWLDAPFPNVTIHHLLHHSGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYFDEETTDDFEDLWKDVPMYHLRRLKDFLPLFQHAPWKFPPGHRFHYNNAGFILLGL
VVESVSGVTFQEYVEANVFQRAGMHESGYFAFDTLPAKTALGYIDLEDGSWKTNLYSL
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LIDREKOBOLLEVLEKKRDEGDITYHI"
COMPLement [2882. 3367]
/gene="BH2270"
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(E-mail:takamih@jamstec.go.jp,
URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html,
Tel:81-468-67-3895, Fax:81-468-66-6364)
On Jan 31, 2001 this sequence version replaced gi:10174886.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MVKKVGLIVGVFALSIGLMACNGQEQEEVEKNIDGEASGEIPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ABC transporter (ATP-binding protein)"
/protein_id="BAB05989.1"
/db_xref="GI:10174890"
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                                                                                                                                                                                                                                                                                                                                                      /product="penicillin-binding protein"
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/db_xref="GI:10174887"
                                                                                                                                             /organism="Bacillus halodurans"
/db_xref="taxon:86665"
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/db_xref="GI:10174889"
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/gene="BH2268"
/note="BH2268
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/gene="BH2269"
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/gene="BH2270"
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/gene="BH2271"
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/transl_table=11
/product="dipeptidase"
                                                                                                                                                                                               /note="alkaliphile"
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                     104. .1102
/gene="BH2267"
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HGDGTDLCSIINGKSGRCGEDCARCAQSKYHKTNISEYPLLDYEKIKKVAKENEDEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"228 aa, similar to sp:BIOD_METJA DETHIOBIOTIN
SYMTHERABE (EC 6.3.3.3) (DETHIOBIOTIN SYMTHASE) (DTB
SYNTHERASE) (DTBS) from Methanococcus jannaschii (248 aa);
33% identity in 221 aa overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRFSIVTSGRGLYGEEFERVITYYSNLNKELKINLCASHGIINKESLIKLKKAGVKRY
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KNFGENAFKAGANATITGNLLTTCGNKIKDDKRLIENIGMRIF"
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Shimizu,T., Ohtani,K., Hirakawa,H., Ohshima,K., Yamashita,A., Shiba,T., Ogasawara,N., Hattori,M., Kuhara,S. and Hayashi,H. Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                Direct Submission Submission Submission Submitted (15-FBB-2001) Tohru Shimizu, Institute of Basic Medical Submitted (15-FBB-2001) Tohru Spattment of Microbiology; 1-1-1 Tennohdai, Tsukuba, Ibaraki 305-8575, Japan (E-mal: tshimizuemd.tsukuba.ac.jp, Tel:81-298-53-3354, Pax:81-298-53-3354, On Jan 14, 2002 this sequence version replaced gi:18145205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="319 aa, similar to pir:B70384 biotin synthetase (2.8.1.6) from Aquifex aeolicus (332 aa); 43.4% identity 311 aa overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in 173 aa
and 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="184 aa, similar to sp:BIOY_BACSH BIOY
                                                                                       . Natl. Acad. Sci. U.S.A. 99 (2), 996-1001 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gangrene"
                                                                                                                                                                                                                                                                                                                                                                                                 perfringens str. 13"
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/transl_table=11
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/protein_id="Bab81250.1"
/db_xref="GI:18145207"
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/transl_table=11
/product="biotin synthase"
/protein_id="BABB1251.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:195102"
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                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="13"
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                                                                                                                                                                                                       209775
                                                                                                                                                                                                                                                                                                                                                                                                 GTCGTTGATGCGATGACAGGGCAAGATGCGGTTAATGTGGCGGGAAAGCTTCCATGAGCAG 209715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACCAGCTCGAACCGTTCCACCCAGAGCGAATGGCTTCGCGGATTCTTGGGATGGGGGAT 209535
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                                                                                                                                Db 209954 TITAGCCTTGGTGATCAAGTAAGCCCTGTTGAAATTGCGAAACAGGCGATCGAGGGGGG 209895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCGATGITTCCGGCGTGTTTTGACGAAGCTGGATGGGGATACTCGAGGCGGAGCTGCC 209655
                                             210014 TATCGTCCGGCTGCGATTAAACAGCTTGAGACATTAGGTAAACAATTAAACATGCCTGTG 209955
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Clostridium perfringens str. 13
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1081 AAAGGGCTAGATAAGCTTAATATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATC 1140
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    TAICGICCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTA 480
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                                                                                         481 TACAGTGAAGGAGATCAAGTAAAGCCACAACAAATTGTAACTAATTGCATTAAAACATGCT
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AMAMAKI I ISKGLODKDFINKYVLGFOEYKDHLENFDLDYLSDECGIEIEDIEKLFKY
YCEKNSSIYLGYGMOKYKNGGNTIRALDALGALFGQIGVKGGGVNYANKVLSRILDSD
PFKSGEVGENREFYVSNINEFIEEPKKYSLSVEDSNAPIKIMYIANSNLANQLPNLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPLMSFENFYPTVDIVKSLIHNEKOLEIDKEKLLVISPDTGAMDRAIYISSVLGYDVG
LEYKRRHBSRIVMGKNPTYHEKYMEKRYDGKDVLIVDDMIASGESVLDIAKELKGRNA
RNYVATTPRFPTECLEKENKFENGTIKKYYSTNLTYIPBELNAAPWFKAVDLSDFI
ARIINRLNYDKSVASYMDATNIIQRLLDEK"
                                                                                                                             SQYGSGGVLKGIEDIFFNFYGGVSKATGGPCWSAGMRAQKYDFGDSVSNSLEDMINSK
NIFLWGKNPANTTIHTMAILNKAKKNGSRIIVIDPINTQSAKLGDIHVKIKPGTDGAL
                                                                                                                                                                                                                                                                                                                                                      LNNSIDKVEFKVCFDMFMIDTASKCDLFIPCTNTLESEDMVFSSMTNPYLLYNEKIIE
PREKLMDEYYFFRELAKRMNLKGYPSLSKKDYLSKVIEPLMSYNKDITLLDYLKNNPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                          VYDDVAWENKKFKTPSGKFELASKRALKECGSLTPTVLSPRIKENCFRLLTNHSKDSL
SSQHYIDVDEKAKVYLNENMIRRFSLICGEKVKLKSRTGEITAICSLDNGVQDYVALM
YVGWWKKHGNPNFLIESGISDMGGQITYNETFIEIENI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFSNGEGKVKIPQSVRGRDIYILCDIGNYSCTYKMFGFENHKGPDEHFQDIKRTVSAI
RGKARRITVIMPLLYESRQHRRKGRESLDCALALQELERLGVDEVLTFDVHDPNVQNA
                                              /translation="MEVLSHGCTLDCFDCCKFNVYKEGSEILKIEGDKEHPFTKGLIC
                                                                                   KKGVAHLNRLNHKDRIYTPLLKNNGVWEEISFEDALEIMKEKLEYTKEKYSSKSILYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MNEQNHGLGITALESCTELGNAIDKLIQEKRNCEESFLIKTDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 185046 ATGGCTTTTGATGGATTAGCGTCTAAATTACAAGACACGCTTAAAAATTAAAGGGTAAA 184987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 184926 GAGGCAGATGTTAACTTCAAGGTGGTAAAAAGTTTATATCAAATGTTAAAGATAAATT 184867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 184866 GTTGGTGAGGAAGTATTAAATAGTTTAACTCCAGGTCAACAGGTTATTAAAAATAGTTAAAT 184807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DD 184806 GACGAATTAACAACTCTTATGGGAGAGACTGAGAGTAAATTAATAATACTCAGACAATGGA 184747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 184986 GGTAAGCTAACAGAAAAAGATATAAAAGCAGAAGCCATGAGAAAGTAAAGCTTGCGCTTTTA 184927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphoribosyl pyrophosphate synthetase (prs) from Treponema pallidum (421 aa); 32.3% identity in 325 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCATTTGAAGGCTTATCAGAACGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GAGGCTGACGTAAACTTTAAAGTGGTAAAAGAATTTATTAAAAACAGTATCAGAACGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATAGTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 CCTACTGTTGTTATGATGGTTTGGTTTACAAGGTGCTGGTAAAACAACAACAGCGGGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GAJGAATTAACGAAGTIGAIGGGTGGAGAAAATACAICGATTAATAIGTCAAATAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 296750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
/product="probable phosphoribosyl pyrophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pir:A71345 probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="353 aa, no significant homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="BAB81256.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 522.8; DB 7.1e-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(11177. .12238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(11177. .12238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB81255.1"
/db_xref="GI:18145212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="CPE1550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CPE1550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10033. .11127
/gene="prs"
10033. .11127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.2%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="prs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 836; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPE1549"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELYMENTERE TWENTER THE NUMBER TO THE THEORY OF THE THEORY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="Mloknifverkomvnkeliengffkiekkineepiggktfnkel
CDYFKEKIEEDSKGILLIVEERDIFKNSVLKYFFEELNYYKFVKNSKIDEIDLAAVKF
NLGYNAFLFDIXEKLNNDSQCLVFKNTDKASEDILNVLSGISPNSCIMLKDNYVIKNK
                                                                              İLLGAKRGALAQIIYYLVGLLGIPVFTQGGGPSYVFQPTFGYLLGFIFGAYIIGKITE
NLKTINIKNLFLAGILGLLVIYLFGVSYMYVIXNFYLGDAMSLLSAVSIGALACLPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKVLCGAIVSTFWFGMATPVFAQSEKTEAVVTLGANLTKSERLQ
MLDAFGVKANEVKIIDVTNQDIREQLGLDTSKPIPASSQSISSSYVVVEDKGGINVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEAAREEISLTNNLSNAKTKDGQTLGKDEAAVVVNJIKTDVIKDKPKNDEEIGKIVNN
VINNYNILLTGGQQGQTIKFMSKINDLDYNYGAMKESLNQMNDKLQQILKDTGKQLEE
SGLLEKALNGIKNVLVDIKDFLVNMFSSASEKVKDGITYDENGNIVIKTGNNSDESKN
EESIQDKEQTQSNDNNQNGENEGGQNQTK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSFVSDIPGETSKKTEEKFKEALGGVLFIDEAYTLANDSIGREAIETLLKLIEDYSRE
VIVILAGYEEEMENFPDVNIGLRSRFPLWTKFEDYNPNELLEMAIKLVEAKGFKLSKN
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IKAMNAIKYDNHFDLEKKLNNLIGNEELKDFIRGQYKLAKIREKRKKLGFQVDLNKYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNLTEVTGSMLANALLTSGVNNADVKADAPFKVTGTAALAGILKGFEDASGEELSLPK
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                                         /translation="MKMKTRDLTLIPIFAALTAIGAFIKIPIPIVPFTLQYFFCALGA
                                                                                                                                                                                                                                                                                                                                                                                  /gencologists as, similar to sp:rPUA_BACSU HYPOTHETICAL 31.3
KDA PROTEIN IN LYSA-PPIB INTERGENIC REGION (ORFX19) from
Bacillus subtilis (290 aa); 31% identity in 271 aa
overlap. Putative N-terminal signal sequence was found by
PSORW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLVEAEEIDEDIVNKIICNNKFFIFLYNKDKGEELEIIDNEFLINKDKTLYRKALSEK
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complement(7634. .9622)
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//octe="1145 aa, similar to gp.AB015670_7 Bacillus sp.genes for CDase, CGrase, MBP and 15 ORFS, partial and complete cds from Bacillus sp (549 aa); 45% identity is 522 aa overlap.Also similar to pri:2516401x stage V sporulation protein K from Bacillus cereus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="conserved hypothetical protein" /protein_id="BaB81252.1"
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/protein_id="Bab81254.1"
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/protein_id="BAB81253.1"
/db_xref="GI:18145210"
                                                                                                                                                                      LLLTFIISLVGSKVCPRLKRFDYI"
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/gene="spoVK"
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/db_xref="GI:18145208"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                      /qene="CPE1546"
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[ [bases 1 to 10173] Smoot, L.M., Smoot, L.M., Smoot, L.M., Smoot, L.M., Chaussee, M.S., Sylva, G.L., Sturdevant, D.E., Ricklefs, S.M., Porcella, S.F., Parkins, L.D., Beres, S.B., Campbell, D.S., Smith, T.M., Zhang, Q., Kapur, Y., Daly, J.A., Veasy, L.G. and Musser, J.M. Groome sequence and comparative microarray analysis of serotype MIS group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKRFFDWLMDADLTQAPKIADIDLSTLEHLTKKDLEAFVÏYLRERPSLNTYSTKEGIS
QTTINRTLSALSSLYKYLTEEVENDQGEPYFYRNVWKKVSTKKKKETLASRAENIKQK
LFLGDETLAFLDYVDKEYEQKLSNRAKSSFRKNKERDLAIIALLASGVRLSEAVNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKDVNLNMMIIEVIRKGGKRDSVNVAGFAKGYLESYLAVRORRYKAEKQDLAFFLTEY
RGVPNRMDASSIEKMVGKYSEDFKIRVTPHKLRHTLATRLYDATKSQVLVSHQLGHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MRRELLLEKIETYKAIMPWYVLDYYQSKLAIPYSFTTLYEYLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MFSGHOLKTARLSKGITOSELGRLLHVNKMT1SNWEKGKNIPNE
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                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 10173)
Smoot,J.C., Barbian,K.D., Van Gompel,J.J., Smoot,L.M.,
Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,
Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M.,
Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.George. and Musser,J.M.
Direct Submission
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putative signal recognition particle -inhibited division
protein [Streptococcus pyogenes MI GAS]"
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/gene="spyM18_1147"
/note="best blastp match gb|AAK34058.11 (AE006560)
putative integrase/recombinase [Streptococcus pyogenes]
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/gene="%pyM18_1150"
/note="best blastp match gb|AAK34059.1| (AE006560)
putative repressor protein [Streptococcus pyogenes M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathogenesis/Rocky Mountain Laboratory of Human Bacterial Pathogenesis/Rocky Mountain Laboratories/NIAID/NIH, 903 S. Hamilton, MT 59840, USA
                                                   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002)
21927593
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/strain="MGAS8232"
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/db_xref="GI:19748306"
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/product="putative repressor protein"
/protein_id="AAL97766.1"
/db_xref="GI:19748307"
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Submitted (31-JAN-2002) Laboratory
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/gene="ffh"
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                         pyogenes MGAS8232
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/gene="spyM18_1147"
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1913. .2611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                            Db 184569 TTCTCAATGGGAGATAAGGTTAAGGCTGTAGATATTGCCAAAGCTGCAATAGAGCATGCA 184510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD 184209 AGTGATATTGAAGTATTCCATCCAGATAGGATTGGCTTCAAGAATATTAGGGAAGAT 184150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1021 GTGAAAAATCTAGGACCACTGGATGATATTATGAAAATGATTCCAGGTATGAATAAAATG 1080
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                                                                                                                                                                                             TACAGTGAAGGAGATCAAGTAAAGCCACAACAAATTGTAACTAATGCATTAAAACATGCT
                                                                                                                                                                                                                                                                                            AAAGAAGAACATTTAGACTTTGTAATCATTGATACAGCAGGTCGATTACACATCGATGAA
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                                                                                            TATCGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTA
                                                                                                                                                                                                                                                                                                                                                                                           GCATTGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAAACCAAACGAAATTATGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNEAYFQKLMTTYGDKAYLHLAKVNIPQKLDQYRQQLILINQDITRTQAHQKKRLKKL
BDQKASLERYITEFEGFTDQYPEEVVVAGILSISYGNVMEMLYAGMNNDFKKFYPQYL
LYPNVFQDAYQDGIIWANMGGVEGSLDDGLTKFKANFAPTIEEFIGEFNLPVSPLYHI
                                                                                                                                                                                                                                                                                                                                                                GKFGLNIIRVDASKRFLDLLADVEDPEKRKIIGNEPVYVFODEASKLKGYDFLAQGT
LYTDIIESGTETAQTIKSHHNVGGLPEDMQFELIEPLNYLFKDEVRALGIALGMPEEI
VWRQPFPGPGLAIRVMGAITEEKLETVRESDAILREEIAKAGLDRDVWQYFTVNTGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVGVMGDGRTYDYTIAIRAITSIDGMTADFAQLPWDVLKKISTRIVNEVDHVNRIVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKALFIKYDPAILLKQYALGQEEEEKPLALAAIKNLQEAGVHWTGLTMEIADSIQPRF
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                                                                                                                                                                                                                                                    TAQELREINPIGIVLSGGPNSVYADNARGIDPEIFELGIPILGICYGMQLITHKLGGK
VVPAGQAGNREYGQSTLHLRETSKLFSGFPQEQLVLMSHGDAVTEIPEGFHLVGDSND
                                                                                                                                                                                                                                                                                                              CPYAAIENTEKNLYGIQFHPEVRHSVYGNDILKNFAISICGARGDWSMDNFIDMEIAK
                                                                                                                                                                                                                                                                                                                                           IRETVGDRKVLLGLSGGVDSSVVGVLLQKAIGDQL1CIFVDHGLLRKDEGDQVMGMLG
                                                                                                                                                                                                                             /translation="MTEISILNDVQKIIVLDYGSQYNQLIARRIREFGVFSELKSHK:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   putative antimicrobial resistance factor [Streptococcus pyogenes MI GAS]"
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putative GMP synthase [Streptococcus pyogenes ML GAS]"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4308 ATGGCTTTTGAAAGCTTAACCCAACGTTTGCAAGAIGTGTTTAAACACACTTCGCGGTAAA 4249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4248 AAGAAATTATCAGAATCAGATGTTCAAGAAGTGACAAAAGAGATTCGTCTAGCTCTTTTA 4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4068 GAAGAATTAACGAGTATTTTAGGCTCAGAAACTGCAGAATTGATAAATTCTCCAAAAATT 4009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAACTATTATCATGATGGTCGGTTTGCAAGGGGCTGGTAAAACAACTTTTGCAGGAAAA 3949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3948 CTCGCTAATAAATTAAATAAAGAAGAAGATGCGCGACCACTGATGATTGCTGCCGATATT 3889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATAGTTCAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GGTABACTTACTGARGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGAATTAACGAAGTTGATGGGTGGAGAAAATACATCGATTAATATGTCAAATAAACCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCIACTGTTGTTATGATGGTTGGTTTACAAGGTGCTGGTAAAACAACAACAGCTGCAGGTAAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="spyM18_1156"
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/note="spyM18_1156"
/note="best blastp match gb|AAK34065.1| (AE006560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGCATTTGAAGGCTTATCAGAACGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 499.2; DB 1;
Pred. No. 1.5e-74;
0; Mismatches 508;
                                                                                                                                     synthase"
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                                                                                                                                     /product="putative GMP sy/
/protein_id="AAL97771.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(8738, .9961)
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61.3%;
/gene="guaA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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TWGIVERSKDQOPRYHIGQAIQVOKSGPYHQWIGTINKOVEDIABNYRVSYHEVVFP
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IGGYQYDINLKDHOLSLOGISEQDFVKPPYIRFWGNGPEQUNRLLERRAFRYAKQHPNS
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NLVTJGFWFRANDLKKODHFMIMADHGTDWHITDNKFTWHRIKRUSHIFDLGSLOGNSLF
EKNOFIGYAPELYODQULSKAQGHDFFSEVIQFDAVHHFAWDGGLLSNIAPNYEAF
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IIMMYGLQGASTABINTERGARLANKLIFEBDARFLMIAADIYRPAAIDQLKTLGQINVPY
PDMGTDHSAVDIYVRGLEQARSHNDYYLIDPAGRLQIDEKLMEELRDYRALAQPNEI
                                                                                                                                                                                                                                                                                                      GERITDIETFHPDRMSSRILGMGDLLTLIEKASQEYDEKKSLELAEKMRENTFDFNDF
                                                                                                                                                                                                                                                                                                                                   IEQLDQVQNMGPMEDLLKMIPGMAGNPALANIKVDENQIARKRAIVSSMTPAERENPD
LLNPSRRRRIAAGSGNSFVEVNKFIKDFNQAKSMMQGVWSGDMSKMMKDMGINPNNLP
                                                                                                                                                                                                                                                                                                                                                                                       KNMPAGMPDMSSLEGMMGQGGMPDLSSLGGDMDMSQLFGGGFKGKIGQFAMKQAMKRQ
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Adefgvsroavydnikrfekiletyemklhmysdyvvrseifddmiahyphdeyloek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQAITLLVBEGILERRIGSGTYVASHRVQEKMRGTTSFTEIIRSQGRQPSGKLLSYQK
QLASDTEVKELNLDKTDLVIRMERIRYADSVPLVYEIASIPEKFIKTVKRADITEHFF
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QYIGDRFEFYLENN"
                                                                                                                                                                                                                                                                              LLVVDSMIGQEAANVAYEFNHQLSITGVVLTKIDGDTRGGAALSVREITGKPIKFTGT
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/product="putative signal recognition particle -inhibited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         putative DNA-binding protein [Streptococcus pyogenes MI GAS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="best blastp match gb|aAK34063.1| (AE006560)
hypothetical protein [Streptococcus pyogenes MI GAS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="best blastp match gb|AAR34062.1| (AE006560) putative transcription regulator, GntR family [Streptococcus pyogenes MI GAS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="best blastp match gb|AAK34061.1| (AE006560)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKLISWFMEPIHFPPNSPVIVAGNIIN"
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/gene="spyM18_1153"
complement(4753, .5451)
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/note="hort"
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/db_xref="G1:19748308"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="spyM18_1152"
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7134. .8696
                                                                              division protein"
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/translation="mkaankalksysnlsdwklysastgamttalddatknytayda
Awsphwmfakyklkylkdskkdfgstbsthsttrkglkkdipfkanktidkfnwtdkdm
BaymldinnGwspbkaakkwikehpkkyaswtsnk"
                                               1 (bases 1 to 4152)
Gutlerrez,J.A., Crowley,P.J., Brown,D.P., Hillman,J.D., Youngman,P.
and Bleiweis,A.S.
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Gutterrex.7.A. and Bleiweis,A.S.
Obtrect Submission
Submitted (04-FEB-1997) Oral Biology, University of Florida, P.O.
Box 10044, "DAMEC, Gainesville, FL 32610-0424, USA
F. (bases 1 to 4152)
Kremer,B.A.H., Crowley,P.J., Gutlerrez,J.A. and Bleiweis,A.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="putative glycinebetaine-binding protein"
/note="synonym=OpuAC; component of an ABC transport sys
involved in the osmoregulated uptake of glycinebetaine"
                                                                                                                                                                                                                                                                   (bases 1 to 4152)
Gutierrez,J.A., Crowley,P.J., Cvitkovitch,D.G., Brady,L.J.,
Hullman,J.D. and Bleiweis,A.S.
Streptococcus mutans ffh, a gene encoding a homologue of the Subunit of the signal recognition particle, is involved in resistance to acid stress
Microbiology 145 (Pt 2), 357-366 (1999)
                                                                                                              Insertional mutagenesis and recovery of interrupted genes of Streptococcus mutans by using transposon Tn917: preliminary characterization of mutants displaying acid sensitivity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kremer, B.H., van der Kraan, M., Crowley, P.J., Hamilton, I.R., Brady, L.J. and Bleiweis, A.S.
Characterization of the sat operon in Streptococcus mutans: evidence for a role of Ffh in acid tolerance
J. Bacteriol. 183 (8), 2543-2552 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (31-00T-2000) Oral Biology, University of Florid
SW Archer Rd, Gainesville,, FL 32610, USA
Sequence Update by submitter
On Oct 31, 2000 this sequence version replaced gi:1850604,
Location/Qualifiers
  3acteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; unique
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/strain="JH1005"
/db_xref="taxon:1309"
                                                                                                                                                                                                     Bacteriol. 178 (14), 4166-4175 (1996)
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/transl_table=11
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/protein_id="AAB48048.1"
/db_xref="G1:1850605"
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/protein_id="AAB48049.1"
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U88582

U88582. GI:11055962
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                            1021 GTGAAAAATCTAGGACCACTGGATGATATTATGAAAATGATTCCAGGTATGAATAAATG 1080
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TATCGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTA
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                                                                                       481 TACAGTGAAGGAGATCAAGTAAAGCCACAAAAATTGTAACTAATGCATTAAAACATGCT
                                                                                                                     TITGATATGGGGACAGACCACTCAGCAGTCGATATTGTCAGAAAAGGTTTGGAACAGGCT
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                                                                                                                                                                                                                                                                                             LLVVDSMIGQEAANVAREFNQQLEVTGVILIKIDGDTRGGAALSVRQITGKPIKFTGT
GEKITDIETFHPDRMSSRILGMGDLLTLIEKASQDYDBQKSAELAEKMRENSFDFNDF
IEQLDQVQNMGSMEDILKMIPGMANNPALANVEVDEGEIARKRAIVSSMTPEERRUPD
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NNADSSALEGYMGQGGMPDMSGLSGANMDVSQMFGGGLKGKVGEFAMKQSMKKMAKRM
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VSSALSKSGSTAIHLPNGIHEIRVTYYTTAVARVAFAISIIVIIVTIIYAVLYHLIEK
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IIMMVGLQGAGKTTPAGKLANKLVKBENARPLMIAADIIYRPAAIDQLKILGQQINVPV
FDMGTEHSAVEIVSQGLAQAKENRNDYVLIDTAGRLQIDEKLMTELRDIKALANPNEI
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PAYWHARAAIDYIHDKNDYGSNHLAVDLEDTETSQQINAILAACBFIKSKWTVTQYEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDGLLQAGIYEEKFSHKKMAEKLDLSPSSFNKRLKSSGLKIYLRNKKVATTLLLNAIR
                                                                                                                        /note="similar to 54 kDa subunit of signal recognition
particle"
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Pred. No. 4e-74;
0; Mismatches 508;
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'db_xref="GI:1850606"
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3828. .>4152
                                                      /gene="ffh"
969.
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Best Local Similarity 61.2%;
Matches 802; Conservative
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/gene="ffh"
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969 ATGCCTTTTGAAAGTTTAACCGAACGTTTACAAGGTGTCTTTAAAAATTTACGCGGCAAA
                                                                   1089 GAAGCTGATGTCGCCTTACCTGTCGTTAAAGAATTTATTAAGCGTGTTCGTAAACGCGT
                                                                                                                                                                                                                  181 TTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATAGTTCAA
                                                                                                                                                                                                                                                                                                     GATGAATTAACGAAGTTGATGGGTGGAGAAAATACATCGATTAATATGTCAAATAAACCA
                                                                                                                                                                                                                                                                                                                                           1209 GAAGAACTGACAGCAGTCCTCGGCTCTGAAACGGCTGAAATTGAAAATCGTCTAAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 TATICGTCCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 TACAGTGAAGGAGATCAAGTAAAGCCACAACAAATTGTAACTAATGCATTAAAACATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1449 TTTGACATGGGGACAGAGCATTCAGCAGTTGAGATTGTAAGTCAAGGTCTGGCTCAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGAAGAACATTTAGACTTTGTAATCATTGATACAGCAGGTCGATTACACATCGATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GITGICGATICAATGACGGGTCAAGAIGCTGTCAATGITGCAGAATCITITGACGAICAA
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Search completed: February 24, 2003, 23:49:03 Job time : 5411 secs

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February 24, 2003, 20:04:35; Search time 260 Seconds (without alignments) 11848.976 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:**
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| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:**
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5.1.4_p5_4578
Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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1368
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Perfect score:
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Maximum DB seq
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                                                                                                                                                                                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	S. aureus ffh codi	Staphylococcus aur	Staphylococcus aur	Staphylococcus aur	S. aureus ffh codi	Staphylococcus epi	Staphylococcus aur	Listeria innocua c	Listeria monocytog
SUMMARIES	~	AAS55331	AAS54393	AAS51783	AAX27222	ABN92495	AAS49372	ABQ67194	ABO70511
<b>a</b>	20	23	23	23	20	24	23	24	24
% Query re Match Length DB	100.0 1368	1368	1368	1365	792	1014	721	319630	2256
% Query Match	100.0	99.3	98.2	98.0	57.8	54.3	51.4	51.2	51.0
Score	1368	1356.8	1344	1341	790.4	743.2	703.4	700.8	697.6
Result	m	7	m	4	S	9	c 7	80	თ ს

Staphylococcus aur Enterococcus faeca		Enterococcus faeca	Staphylococcus aur		Streptococcus poly		Streptococcus pneu	DNA encoding Strep	tococcus	-cn	sptococcus	CFE 28 coding sequ		Bacillus lichenifo	S. pneumoniae deri	Streptococcus pneu	Staphylococcus aur	Haemophilus influe	Haemophilus influe	Staphylococcus aur	Buchnera sp. genom	enomic	E. coli growth and	E. coli DNA for ce	Salmonella typhi D	N. meningitidis pa	Neisseria meningit	Neisseria meningit	Staphylococcus aur	Pseudomonas aerugi	Borrelia burgdorfe	Ehrlichia sp. E74	Staphylococcus aur	Nucleotide sequenc
AAV75400 AAS51308	AAS53127	AAX12974	AAS49408	AAS49436	ABN67087	AAS55790	AAX19484	ABK48379	AAS55519	AAH90837	AAV52179	AAH90724	ABN67088	ABK74556	AAZ96317	AAV42992	AAS50493	AAS53231	AAT42063	AAV75697	ABA92787	AAF28549	AAH84550	AAS52529	3	AAA81483	AAF21544	AAF21607	AAS49670	AAS54213	AAX20248	AAV65141	079	AAX91990
18	23	20	23	23	24	23	20	24	23	22	13	22	24	24	13	13	23	23	17	18	24	22	22	23	23	21	21	21	23	23	20	20	23	20
644 1416	1434	6729	521	521	1563	1395	1569	1569	1572	1605	7577	1572	1563	1136	2026	2026	468		1830121		640681	92407	1362	1362	1506	8367	349980	349980	330	1374	910715	4804	292	1230025
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612.4 568.6	568.6													486.4	477.6				443.4	433,8	418.2	404	370.6	370.6	360	341.4	341.4	341.4	328.4	280		Ñ	m	60.
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## ALIGNMENTS

RESULT 1

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Efh gene; signal recognition particle; SRP; antimicrobial agent; vaccine; immunological response; gene therapy; infection; otitis media; conjunctivitis; toxic shock syndrome; septic arthritis; ss.
                                                                                                                                                                                                                                                                                                                        New Staphylococcus aureus Signal Recognition Particle (SRP) with
                                                                     S. aureus ffh coding seguence.
       AAX27221 standard; DNA; 1368
                                                                                                                                                                                                    98EP-0306741.
                                                                                                                                                                                                                       97US-0927216.
                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM.
                                                 (first entry)
                                                                                                                                     Staphylococcus aureus
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P-PSDB; AAY00910.
                                                                                                                                                                                                                       10-SEP-1997;
                                                                                                                                                                                                   24-AUG-1998;
                                                                                                                                                         EP902087-A2.
                                                 28-MAY-1999
                                                                                                                                                                              17-MAR-1999.
                                                                                                                                                                                                                                                                  Wallis NG;
                             AAX27221;
AAX27221
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particle (SRP) if hoomponer. Frh polynucleotides are useful for diagnosing a disease related to expression of fih polypeptides by analysing for the presence/amount of fin protein in a sample due to infection of a micro-organism with the gene, or determining the nucleic acid sequence encoding fih. Fih polypeptides and antagonists are useful for treatment of an individual in need (polypeptide) of, or needing to inhibit (antagonist) fih polypeptide levels. Fih polypeptides and polypeptides and polypeptide are useful for identifying agonists and antagonists by binding and observing the affect of fih polypeptides and antiquenic fragments of potential anti-microbial agents. Fih polypeptides and antiquenic fragments are also useful for inducing an immunological response (T cell/antibody) to protect against disease, by direct administration (vaccine), or via a vector (gene therapy). Anti-fih antibodies are useful as antagonists, and for protecting against disease. Diseases diagnosed, prevented and treated include those caused by infection, especially bacterial infection, include those caused by infection, especially bacterial infection, are useful for bathing wounds and implants prior to surgical
                            useful as diagnostic reagents and for prevention and treatment of
Staphylococci infections which cause otitis media, septic arthritis
                                                                                                                                                                                              encodes the Staphylococcus aureus signal recognition
protein (ffh) and RNA (ffs) components - the SRP gene and protein
                                                                                                                                       Claim 1; Page 28; 35pp; English.
                                                                             toxic shock syndrome
                                                                                                                                                                                              This sequence
                                                         Staphylococci
and toxic shoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               implantation
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Sequence 1368 BP; 521 A; 186 C; 288 G; 373 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCGTCCAGCAGCAGTAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTA 480
                                                                                                                          GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT 120
                                Gaps
                                                                                1 ATGGCATTTGAAGGCTTATCAGAACGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAAG 60
                                                              1 ATGCCATTTGAAGGCTTATCAGAACGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAAG 60
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Score 1368; DB 20;
Pred. No. 9.2e-296;
                             0; Mismatches
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Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
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Pred. No. 2.9e-293;
0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                       Trawick JD,
                                                                                                                                                                                                                                                                                                                                 development
                                                                                                                                                                                                                                                                                                                                sotides for the identification and development comprise sequences of antisense nucleic acids
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                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                     Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; Seq ID No 8968; 511pp; English.
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                                                                                                                                                                                                                     Zyskind
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2000US-207727P.
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99.5%;
 2001WO-US09180
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                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC.
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P-PSDB; AAU37472.
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antibiotics, compris
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Best Local Similarity
                                                                                                      27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-0CT-2000;
21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                        Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind JW, Wall D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; Seq ID No 8030; 511pp; English.
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98.9%;
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2000US-207727P.
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2000US-253625P.
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2001US-269308P.
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                                                                                                                                                                 Staphylococcus aureus
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P-PSDB; AAU36534.
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23-MAY-2000;
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27-NOV-2000;
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16-FEB-2001;
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                                    13-FEB-2002
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                                                 Length 1365;
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  Sequence 1365 BP; 518 A; 190 C; 285 G; 372 T; 0 other;
                                              Score 1341; DB 23;
Pred. No. 9.8e-290;
0; Mismatches 15;
                                              Query Match
Best Local Similarity 98.9%;
Matches 1350; Conservative
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The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen a wide variety of organisms. The present sequence is also useful to screen a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form the contract of the printed specification, at the present sequence is also used to the contract of the printed specification, at the present sequence and the patent did not form part form the contract of the printed specification, at the present sequence and the patent did not form part form the contract of the printed specification, at the present sequence and the patent did not form part form the patent did not form part form the present sequence and patent did not form part form the present sequence and patent did not form part form the patent did not form part form the present sequence and patent did not form part form the present sequence and patent did not form part form 
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                                              AACGATATGAAGAAATGATGAAACAATTCACTGGTGGCGGTAAAGGTAAAAAGGTAAA 1320
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                                                                                                                                              1321 CGCAATCAAATGCAAAATATGTTAAAAGGTATGAATTTACCGTTTTAA 1368
                                                                                                                                                                        prokaryotic cellular proliferation gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug design.
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus
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P-PSDB; AAU33924.
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
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16-FEB-2001;
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Yamamoto RT,
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                                                                 1140
                                                                                                                                                                                                     CGTATTGCTAAAGGGTCTGGTCGTTCATTACAAGAAGTCAATCGTTTGATGAAACAATTT 1260
                                                                                                                                                                                                                                       CGTATTGCTAAAGGTTCTGGTCGTTCATTACAAGAAGTCAATCGTTTGATGAACAATTT 1260
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                                                                                                                                                                                                                                                                                                       1261 AACGATATGAAGAAAATGAFGAAACAATTCACTGGTGGCGGTAAAAGGTAAAAAGGTAAA 1320
                              GTGAAAAATTTAGGACCACTGGATGATATTATTAAAATGATTCCAGGTATGAATAAATG 1080
                                                                                                                                   CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACACATTGAATGTATCACGTAAAAG 1200
GEGAAAAATCTAGGACCACTGGATGATATTATGAAAATGATTCCAGGTATGAATAAAATG 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Staphylococcus aureus Signal Recognition Particle (SRP) with protein (ffi) and RNA (ffs) components - the SRP gene and protein useful as diagnostic reagents and for prevention and treatment of staphylococci infections which cause otitis media, septic arthritis
                                                                                     AAAGGUCIAGAIAAGCITAAIATGAGGGAAAAGCAAATTGATCATATTAAAGCGATTATC
                                                                                                                                                       AAAGGGCTAGATAAGCTTAATATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ffh gene; signal recognition particle; SRP; antimicrobial agent; immunological response; gene therapy; infection; otitis media; conjunctivitis; toxic shock syndrome; septic arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                             CGCAATCAAATGCAAAATATGTTAAAAGGTATGAATTTACCGTTT 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aureus ffh coding sequence.
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P-PSDB; AAY00911.
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polynucleotides are useful for identifying agonists and antagonists by binding and observing the affect of ffh polypeptide activity, which are potential anti-microbial agents. Ffh polypeptides and antigenic fragments are also useful for inducing an immunological response (T cell/antibody) to protect against disease, by direct administration (vaccine), or via a vector (gene therapy). Anti-ffh antibodies are useful as antagonists, and for protecting against disease. Diseases diagnosed, prevented and treated include those caused by infection, especially bacterial infection, including otitis media, conjunctivitis, toxic shock syndrome, wound infection and septic arthritis. Ffh polypeptides are antimicrobial, and are useful for bathing wounds and implants prior to surgical
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                                                                                                                                                                                                 Sequence 792 BP; 296 A; 116 C; 164 G; 216 T; 0 other;
                                                                                                                                                                                                                            Score 790.4; Pred. No. 6e-100; Mismatches
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   GATGAATTAACGAAGTTGATGGGTGGAAAAATACATCGATTAATATGTCAAATAAACCA 300
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                                                                                           TACAGTGAAGGAGATCAAGTAAAGCCACAAAAATTGTAACTAATGCATTAAAACATGCT
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Antisense; ss; prokaryotic cel
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Antisense; ss; prokaryotic cel
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Staphylococcus aureus.
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PF 21-MAR-2001; 2001WO-US09180.
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W.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                           Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATAGTTCAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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                                                                                                                                                                                                      Staphylococcus epidermidis ORF nucleic acid seguence SEQ ID NO:1958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGCCATTTGAAGGCTTATCAGAACGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 743.2; DB 24; Length 1014;
Pred. No. 2.2e-156;
0; Mismatches 158; Indels 0;
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nilarity 84.1%;
Conservative 0
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Matches 838; Conserv
781 TTATCTATTCGT
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                                                                                                                                                                                                                                                             antibacterial;
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601 GCATTGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAACCAAACGAAATTATGTTA 660
353 TIAGCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGCAGCAGATATT 294
                                                                                                                                                                                                                                                173 AAAGAAGAACATTTAGACTTTGTAATCATTGATACAGCAGGTCGATTACACATCGATGAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators
                                        421 TATCGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTA
                                                                                 293 TATCGTCCAGCAGCATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTA
                                                                                                                                             113 GCATTGATGAACGAATTAAAAGAAGTAAAAGACATTGCTAAACCAAACGAAATTATGTTA
                                                                                                                                                                                                          541 AAAGAAGAACATTTAGACTTTGTAATCATTGATACAGCAGGTCGATTACACATCGATGAA
                                                                                                                          481 TACAGTGAAGGAGATCAAGTAAAGCCACAACAAATTGTAACTAATGCATTAAAACATGCT
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                                                                                                                                                                                                                                                                                                                                                                       661 GITGICGATTCAATGACGGGTCAAGATGCTGTCAATGTTGCAGAATCTTTTGA 713
                                                                                                                                                                                                                                                                                                                                                                                              Listeria innocua contig DNA sequence #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ67194 standard; DNA; 319630 BP.
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kunst F, Glaser P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listeria innocua.
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                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The prokaryotic development. The identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention is also useful for the inferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense
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                                                                                                                                                                                                                               Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGGCATTTGAAGGCTTATCAGAACGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                               Trawick JD,
                                                                                                                                                                                                                                                                                                                                New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
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Pred. No. 1.5e-147;
0; Mismatches 6;
                                                                                                                                                                                                                               Zyskind JW, Wall D,
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Seq ID No 1949; 511pp; English.
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
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ilarity 99.2%;
Conservative (
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                                                                                                                                                                                                                               Ohlsen KL,
                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                     Xu HH;
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707; Conserv
                 21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
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22-DEC-2000;
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Yamamoto RT,
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(ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of agene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication
                                                                                                                                                                                                                                                                                  used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             printed specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-Listeria vaccines.
Note: The sequence data for this patent did not form part
The present invention relates to nucleic acid sequences
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                                                                                                                                  121 GAGGCTGACGTAAACTTTAAAGTGGTAAAAGAATTTAATAAAACAGTATCAGAACGCGCA
                                                                                                                                                                             TTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATAGTTCAA
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                                                                                                                                                                                                                                                                                                       361 TTAGCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGCAGCAGATATT
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        Length 319630;
                             0;
                             Indels
         DB 24;
       Score 700.8; DB 24;
Pred. No. 2.5e-146;
0; Mismatches 387;
        51.2%;
70.7%;
                            Matches 933; Conservative
                  Similarity
        Query Match
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(ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
Db 189184 GCTGAAARAGAAAAAAAGCAAATGACGAAAGGGGGGGGAAAAGGTAAGAAAGGTAAA 189243
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                                                                                                                                         AAAGGCCTCGACAACATGCAAGTAGATGATAAACAACTCGGTCACATCGAAGCGATAATT
                                                                                                                                                                                                      CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACACATTGAATGTATCACGTAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGGGCTAGATAAGCTTAATATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.0%; Score 697.6; DB 24; Length 2256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes 4b contig DNA sequence #453
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ID ABQ70511 standard; DNA; 2256
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Fannon MR,
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Mismatches 389;
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immundetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used Computer readable medium; vaccine; S.aureus infection; immunodetection; callullitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds. 1141 CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACACATTGAATGTATCACGTAAAAAG 1200 467 407 AAAGGGCTAGATAAGCTTAATATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATC 526 AAGTCAATGACAAAATGAAAAAGACAATCCAGATATCATCAATGCAAGTAGAAAAA 466 CGGAITGCACGTGGTAGCGGACGTCCGGTTCAAGAAATTAACCGTCTCCTAAAACAATTT 1261 AACGATATGAAGAAAATGATGAAACAATTCACTGGTGGCGGTAAAAGGTAAAAAGGTAAA Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines 586 AAAGGCCTCGACAACATGAACGTCGATGATAAACAACTAGGTCATATTGAAGCAATTATC 1201 CGTATTGCTAAAGGGTCTCTGGTCGTTCATTACAAGAAGTCAATCGTTTGATGAAAATTT CA; Kunsch

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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                             Haselbeck R,
21-MAR-2001;
                                                               16-FEB-2001;
                                                                                                     Yamamoto RT,
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Matches 844;
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                                                                                                                                    AAGTAAAAGAAATTGCTAAACCAAACGAAATTATGTTAGTTGTCGATTCAATGACGGGTC
                                                                                                                                                                   AAGATGCTGTCAATGTTGCAGAATCTTTTGACGATCAACTTGATGTCACAGGTGTTACCT
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the
                                      Score 612.4; DB 18; Length 644;
Pred. No. 3e-127;
2; Mismatches 9; Indels 2;
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contained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense, ds; prokaryotíc cellular proliferation gene;
antibiotic; antibacterial; drug design.
                      C; 89 G; 232 T; 3 other;
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DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                   homologues of any of the S.aureus computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS51308 standard; DNA; 1416
                                      tch 44.8%;
al Similarity 98.0%;
628; Conservative
                      Sequence 644 BP; 184 A; 136
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                                       Query Match
Best Local Similarity
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella Denumoniae, Pseudomonas aeruginosa and Enterococcus facealls. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins can be used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is also useful to screen can offer nomologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part to the printed specification, but was obtained in electronic
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ilarity 64.8%; Pred. No. 2.1e-117;
Conservative 0; Mismatches 459;
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20000S-207727P.
20000S-242578P.
20000S-253625P.
20000S-257931P.
2001WO-US09180.
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Xu HH;
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Yamamoto RT,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are bachemoniae preumoniae, pseudomonsa seruginosa and Enterococcus facealis. The prokarion is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention is also useful for the antisense nucleic acids can also be used to invention to express these proteins. The proteins used in proliferation, to express these proteins. The proteins and be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part command directly from MIPO at
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antibiotic; antibacterial; drug design.
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                                         GATGAATTAACGAAGTTGATGGGTGGAGAAAATACATCGATTAATATGTCAAATAAACCA
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primary nuclectide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococus faecalis genome with commercial importance. The products can be used to defect the presence of Enterococus faecalis in samples. They can also be used for diagnosing Enterococus Infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAXI2938 to AAXI3919 represent these nucleotide sequences which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3781
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                                                                                                                                                            faecalis; contig; detection; Enterococcal infection;
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                                                                                                                                                                           vaccine; attenuation; computer readable medium; ds
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Pred. No. 2e-116;
1; Mismatches 461;
                                                                                                                            ID NO:37
                                                                                                                             SEQ
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                                                                                                                             faecalis genome contig
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                              BP.
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97US-0044031.
97US-0046655.
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Similarity 64.5%;
11; Conservative
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                              AAX12974 standard; DNA;
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                                                                                                                             Enterococcus
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06-MAY-1997;
16-MAY-1997;
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                                                                      GATGAATTAACGAAGTTGATGGGTGGAGAAAATACATCGATTAATATGTCAAATAAACCA
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prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus almonalla typhi, Klebsiella premuoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                             Staphylococcus aureus cellular proliferation inhibitory sequence #632.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                             4982 AAAGAATCCAAAAAATGATGCAACAAATGTCCAAAGGGGATA 5024
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2000US-207727P.
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2000US-257931P.
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AAS49408 standard; DNA; 521
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Xu HH;
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Matches 518; Conserv
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27-NOV-2000;
22-DEC-2000;
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Yamamoto RT,
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26-MAY-2000;
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antibiotic;
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       AGGGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTAC 462
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                                                                                               AATTAGCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGCAGCAGATA 418
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                                                                 461 ITGAGGCTGACGTAAACTTTAAAGTGGTAAAAGAATTTATTAAAACAGTATCAGAACGCG
                                                       CATTAGGITCCGATGTAATGCAATCATTAACACCCAGGGCAACAAGTTATTAAAATAGTTC
                                                                                       AAGATGAATTAACGAAGTTGATGGGTGGAAAAATACATCGATTAATATGTCAAATAAAC
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New polynucleotides for the identification and development of
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Xu HH;
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The invention relates to antisense inhibitors of genes essential to prokaryoric cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas acrutinosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins capable of binding to the express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense coligonuclochide of the invention.

Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACCTACTGTTGTTATGATGGTTGGTTTACAAGGTGCTGGTAAAACAACAACAACTGCAGGTA 358
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Pred. No. 8.2e-106;
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ID No 2013; 511pp; English.
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99.4%;
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Claim 1; Seq
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US-08-921-527-46

US-09-066-047-6

US-09-021-017B-928

US-09-07-476-1

US-09-134-0112-1980

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Listing first 45 summaries
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Sequence 33, Appl
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Sequence 13, Appl
Patent No. 523168
Sequence 19, Appl
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Patent No. 6284515

GENERAL INFORMATION:

APPLICANT: Black, Michael T.

TITLE OF INVENTION: SIGNAL RECGNITION PARTICLE POLYPEPTIDES

TITLE OF INVENTION: AND POLINUCLEOTIDES

FILE REPRENCE: GARCOSCOPE 1998-03-05

CURRENT FILING DATE: 1998-03-05

EARLIER PILING DATE: 1997-09-03

NUMBER OF SEQ ID NOS: 8
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US-08-46-1378-1

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US-08-44-1378-1

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US-08-47-146-19

US-08-47-1-648-19

US-08-47-1-668-19

US-08-469-34-19

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     TITLE OF INVENTION: SIGNAL RECOGNITION PARTICLE POL
TITLE OF INVENTION: AND POLYNUCLEOTIDES
FILE REFERENCE: GMS5035
CURRENT APPLICATION NUMBER: US/09/035,382
CURRENT FILING DATE: 1998-03-05
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
IENGTH: 792
TYPE: DD NO 3
TYPE: DD NA
CORMANISM: Staphylococcus aureus
                                                                                                                                                                                                                   Score 790.4; DB 4;
Pred. No. 6.2e-191;
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99.9%;
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APPLICANT: Black, Michael
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Sequence 3, Application US/09035382 Patent No. 6284515 GENERAL INFORMATION:

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-09-035-382-3

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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
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61.1%; Pred. No. 2.3e-116;
iive 0; Mismatches 510;
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APPLICATION NUMBER: US/08/923,772
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; Patent No. 5972651
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TITLE OF INVENTION: NOVEL ffh
NUMBER OF SEQUENCES: 2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
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COMPUTER: IBM Compatible
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ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,
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LENGTH: 1569 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 61.1
Matches 802; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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US-08-923-772-1
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US-08-923-772-1
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TITE OF INVENTION: DOUCETTE-STAMM et al
TITE OF INVENTION: DOUCETTE-STAMM AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ DD NO 1958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 743.2; DB 4; Length 1014;
Pred. No. 5.9e-179;
0; Mismatches 158; Indels 0;
                                                                                                                         Sequence 1958, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%;
84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 84.1 Matches 838; Conservative
GENERAL INFORMATION:
                                                                                 RESULT 3
US-09-134-001C-1958
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
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                                                                                                                                                                                                                                                                Sequence 1, Application US/09385287 Patent No. 6350857 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                              APPLICANT: Black, Michael
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STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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61.1%;
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Best Local Simi.
Matches 802;
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US-09-385-287-1
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ATGGCATTTGAAGGCTTATCAGAACGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAAG
                             ATGCCATTTGAAAGTTTAACAGAACGTTTGCAGAACGTCTTTAAAAATCTACGTAAAAA
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
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SOFTWARE FRACESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,287
FILING DATE: 30-Aug-1899
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
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Pred. No. 2.3e-116;
0; Mismatches 510;
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REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10080
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US-08-961-527-46
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STREET: 9410 Key West Avenue
CITY: Rockville
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                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Streptococcus NUMBER OF SEQUENCES: 391
                                                                                                                                                                                     US-08-961-527-46/c
; Sequence 46, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 7577 base pairs
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HP Vectra 486/33
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                                                                                                                                                                                                                                                                                        APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep
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Matches 802; Conservative
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DNESS: double
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ADDRESSEE: Human Gen
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BELTZ, Gerald A.
COUGHLIN, Richard T.
TITLE OF INVENTION: UNCLERC ACIDS, PROTEINS, AND METHODS OF USE OF GRANULOCYTIC ERHLICHIA

APPLICANT: MURPHY, Cheryl

GENERAL INFORMATION:

STOREY,

ADDRESSEE: HALE AND DORR LLP STREET: 60 State Street

CORRESPONDENCE ADDRESS: SEQUENCES:

NUMBER OF

SOFTWARE: Patentin Release #1.0, Version #1.30

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

COUNTRY: United States ZIP: 02109

COMPUTER READABLE FORM:

STATE: Massachusetts

CITY: Boston

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/066,047A

FILING DATE: 24-Apr-1998 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/044,869 FILING DATE: 25-APR-1997 ATTORNEY/AGENT INFORMATION:

106.941.156

ATTORNET/AGENT INFURGATION:
NAME: Superko, Colleen
REGISTRATION NUMBER: 39,850
REFERENCE/DOCKET NUMBER: 106.
TELECOMMUNICATION INFORMATION:
(617) 526-6000

TELEPHONE: (617) 526-60 TELEFAX: (617) 526-5000 INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS

LENGIH: 4804 base

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                                                                                                                                                                                                                                                                                                                                                                                                          CTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTTGAGGCT 126
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                               7 TTTGAAGGCTTATCAGAACGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAAGGGTAAA
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                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                  Length 4804;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                Query Match 19.6%; Score 268; DB 4; L. Best Local Similarity 51.8%; Pred. No. 1.6e-58; Matches 657; Conservative 0; Mismatches 605;
                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                 HYPOTHETICAL: NO
                                                                                                                     ANTI-SENSE: NO
                                                                                                                                                                     0S-09-066-047-6
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; Sequence 6, Application US/09066047A; Patent No. 6306394

RESULT 7 US-09-066-047-6

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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                 OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 706141
INFORMATION FOR SEQ ID NO: 928:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.5%;
ilarity 53.6%;
Conservative (
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1098 base pairs
                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 23-DEC-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                            94304-1018
                                                                      Palo Alto
                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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US-09-221-017B-928
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Local S...
548;
                                                                      CITY: Pal
STATE: CA
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                                                                                                                                                                                                                                                          4093 ATAGATGAGCTGAAGTGTGTAAAGAAGGAGGTATCACCAGCTGAAATTGTATTGGTTGTA 4152
                                                                                                                                                                                                                                                                                                                                                                                                                     4153 GACTCCTTAATGGGGCAAGATGCCGTCACTATGGTGCGCAAGTTCAATGAGGAGTTAGGC 4212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               967 AAGATGCGTGAGTCATCGTTTACTTTAGATGATTTTTTAGAACAACTTGATCAGGTGAAA 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1027 AATCTAGGACCACTGGATGATATTATGAAAATGATTCCAGGTAT---GAATAAAATGAAA 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1084 GGGCIAGATAAGCTTAATATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATCAG 1143
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                                               3855 --ACTGAGGTTAAAGAATGGATTCTAAAAACCCGTTGGTAGCGTCTTTAGACGTATATCGT 3912
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             367 ITAPTIGATGCGTAAAAAATACAAAAAAACCTATGTTAGTTGCAGCAGATATTTATCGT 426
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                                                                                                                                                                                  727 GTCACAGGIGITACCITAACIAAAITAGAIGGIGAIACACGIGGIGGIGCAGCIIIAATCI
                                                                                        CCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTATACAGT
                                                                                                                                                            487 GAAGGAGATCAAGTAAAGCCACAAAATTGTAACTAATGCATTAAAACATGCTAAAGAA
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Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLECTIDES AND USES THEREOF
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4753 CAGATGAA 4760
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1092 GGIGAGGGGAGAATTACCGAGATCAATGTAGCCGAAACTCTCAAAGATGTACGTCGTGCC 1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 TTATTTGAGGCTGACGTAAACTTTAAAGTGGTAAAAGAATTTATTAAAACAGTATCAGAA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1032 CTTTTGGATGCCGACGTGAACTATGTCGTTGCCAAGCAGTTTACGGACTTGGTGAAGGAA 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            972 AAAGCCAICGGCCAAAACGIGCTGACCTCCGICCGTCCGGGCGAACTGAIGGTGAAGATC 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 GTTCAAGATGAATTAACGAAGTTGATGGGTGGAGAAAATACATCGATTAATATGTCAAAT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCGCCATTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATA
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Pred. No. 8.2e-55;
0; Mismatches 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27340-20021.00
                                                                                                                   APPLICATION DATE:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATE:
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PCJ/4U98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
ANNER: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
23-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376
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                                                                                                                                                                                                                                                                                                                                                         774
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                                                                                  CCTGTATACAGTGAAGGAGATCAAGTAAAGCCACAAAAATTGTAACTAATGCATTAAAA 534
                                                                                                                                                                                                                                  675 CCCGTCTACAGCGAACCGGACAGCAAAAGCCGGTCGAGATAGCCCGGACACGCCATAGCC 616
                                                                                                                                                                                                                                                                   594
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295 AAACCACCTACTGTTGTTATGATGGTTGGTTTACAAGGTGCTGGTAAAACAACAACTGCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 ACACGCTIGGATITCGACGGTGTTGTCCTIACCAAGCTCGATGGAGATACCCGGGGCGGT
                   GCCAGTCCGGCAGTAATCCTGATGTCCGGATTGCAAGGTTCGGGTAAGACCACCTTCTCC
                                                              GGTAAATTAGCATTATTGATGCGTAAAAATACAACAAAAAAACCTATGTTAGTTGCAGCA
                                                                                                                                 GATATTTATCGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATT
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APPLICANT: Stadola, Robert
TTLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 180, Application US/08858207A Patent No. 6348328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -08-858-207A-180
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Pred. No. 1.1e-34;
0; Mismatches 169;
                                                                                               SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                   OFENSE: FastSey .... SOFTWARE: PastSey .... SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
                                                                                                                                                                                                                                                                                                                                        P50475
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                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATCGTCCAGCAGCGATAAATCA 443
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P5(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                       38,891
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                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 836 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 274; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                NAME: Gimmi, Edward R
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-270-5090
                                                                            COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
COUNTRY: USA
ZIP: 19406-0939
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US-08-858-207A-180
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US-09-007-476-1
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738 TACCTTAACTAAATTAGAIGGTGATACACGIGGTGCTGCTGCTTTAICTATTCGTTCGGT 797
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0; Mismatches 267
                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1980, Application US/09134001C; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-1980
                                                                                                                                                                                                                                                                                                                                             1242 GGCA 1245
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US-09-134-001C-1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                 ADDRESSE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 145.6; DB 3;
Pred. No. 8.9e-28;
0; Mismatches 309;
                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/007,476
Black, Michael T.
TENTION: No. 6159949el FtsY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GM10079
                                                                                                                                                                                                                                                                                                                                                                                                                                 36,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GM
FELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%;
                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1251 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.6
Matches 388; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 COMPUTER READABLE FORM:
                TITLE OF INVENTION:
                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear US-09-007-476-1
                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                            19103
                                                                                                                                             COUNTRY:
                                                                                                                           STATE:
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION:

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 1980 1068 AFTGCACATTCCAGTTAAATATGTAGGTTTAGGTGAGCAATTAGATGACTTACAACCATT 1127 1128 TAACCCTGAAAGTTATGTCTACGGCTTAT-----TCGCTGATATGATTGACAAATGA 1181 395 635 276 ATCGATTAATAIGTCAAATAAACCACCTACTGTTGTTATGATGGTTGGTTTACAAGGTGC 335 656 455 657 AGTAATGTTAGCCGCTGGTGATACCTTCAGAGCTGGAGCAATTCAACAATTAAACGTCTG 716 717 GGGAGAACGIGIIGGIGIIGGAGIIGIGAGICAAAACGAAGGIICIGACCCIGCAGCAGI 776 896 Gaps 858 CCATCCTGAACGTATGGCATCACGTATTTTAGGTATGGGTGATGTGTTAAGTTTAATTGA 918 AAAAGCGCAACAAGATGTGGATCAAGAAAAAGCAAAAGATTTAGAGAAAAAGATGCGTGA 336 IGGTAAAACAACAGCAGGTAAATTAGCATTATTGATGCGTAAAAATACAACAAAA 600 CGGCAAAACAACAACAATTGGTAAATTAGCTTATCGTTATC---AACAAGAAGGTAAAAA 396 ACCTATGTTAGTTGCAGCAGATATTTATCGTCCAGCAGCATAAATCAATTACAAACAGT 516 TGTAACTAATGCATTAAAACATGCTAAAGAAGAACATTTAGACTTTGTAATCATTGATAC 576 AGCAGGTCGATTACACATCGATGAAGCATTGATGAACGAATTAAAAGAAGTAAAAGAAAT 837 rgcaggacgcrtgcaaaaraaarctaatttaargcaagagrtagaraaargaaacgtgr GACACAAAAACCAATTAAATTTGTTGGTATGAGTGAAAAGTTAGATGGTTTAGAGCTATT 456 AGGGAAACAAATTGATATTCCTGTATACAGTGAAGGAGATCAAGTAAAGCCACAAAAT Query Match 10.6%; Score 144.8; DB 4; Length 1248; Best Local Similarity 54.6%; Pred. No. 1.4e-27; Matches 346; Conservative 0; Mismatches 267; Indels 21;

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313 GACGTGCTGCTGGTGGATACCGCCGGTCGTCTGCATGTTGACGAAGCGATGATGACGAA 254
                                                                    253 ATCAAACAGGTCCACGCTTCTATCAAGCCAGTAGAAACGCTGTTTGTCGTCGATGCGATG 194
                                                                                                                                                                            GITACCITAACIAAAITAGAIGGIGATACACGIGGIGGIGCAGCITTAICIAITCGITCG 795
                                                                                                                                                                                                                                                  796 GIGACACAAAAACCAATTAAATTIGIIGGIAIGAGIGAAAAGITAGAIGGIITAGAGCII 855
                                                                                                         676 ACGGGTCAAGATGCTGTCAATGTTGCAGAATCTTTTGACGATCAACTTGATGTCACAGGT
                                                                                                                                                                                                73 ATCACCGGCAAGCCGAITAAATTCCTCGGTGTCGGCGAGAAAACCGACAGGCGCTGGAGCCA
                                   616 TTAAAAGAAGTAAAAGAAATTGCTAAACCAAACGAAATTATGTTAGTTGTCGATTCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARRE: FastESD for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,484
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NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%;
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LENGTH: 831 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 215-994-2488
TELEFAX: 215-994-2222
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nes 300; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                         856 TICCAICCIGAAC 868
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                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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US-09-007-484-3
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STATE:
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APPLICANT: Mahan Dr., Christopher P.
APPLICANT: Conner Mr., Christopher P.
APPLICANT: Hiethoff Mr., Douglas B.
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION
TITLE OF INVENTION: OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST
TITLE OF INVENTION: INFECTION
NUMBER OF SEQUENCES: 255
CORRESPONDENCE ADDRESS:
                                                                        GGGTCAAGATGCTGTCAATGTTGCAGAATCTTTTGACGATCAACTTGATGTCACAGGTGT
                                                                                                                                                                                                798 GACACAAAAACCAATTAAATTTGTTGGTATGAGTGAAAAGTTAGATGGTTTAGAGCTATT
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Pred. No. 2.3e-23;
0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           Chrisman, Bynum & Johnson, P.C.
                                                                                                                                                                                                                                                                   858 CCATCCTGAACGTATGGCATCACGTATTTTAGGT
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FILING DATE: 17-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Petersen Mr., Steven C.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Chrisman, Bynum & STREET: 1900 Fifteenth Street CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/546-1300
TELEFAX: 303/449-5426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 390 base pairs
nucleic acid
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Best Local Similarity
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TOPOLOGY: li
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US-08-651-155B-4/C
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ZIP: 80302
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556 GACTITGTAATCATTGAIACAGCAGGTCGAITACACAICGAIGAAGCAITGAIGAACGAA 615

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                                280 GC---CCACCGCTACAAACGAACTGGTAAGAAGGTCATGCTGGTTGCAGCAGATACCTTC 336
                                                                      CGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTATAC 483
                                                                                                    337 CGIGCGGGTGCAGTAGATCAGCIAGCIGAAIGGGGCCGACGAGGAGGIAGIA 396
                                                                                                                                       484 AGTGAAGGAGATCAAGTAAAGCCACAACAAATTGTAACTAAATGCATTAAAACATGCTAAA 543
                                                                                                                                                                       397 ACTGGACCTGAAAAGCTGATCCAGCCAGCGTGGTCTTTGATGGTATGGAACGTGCCGTG 456
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GCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGCAGCAGATATTAT 423
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ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 1910
ZIP: 1910
MEDIUM TYPE: Diskette
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APPLICANT: Black, Michael T.
TITLE OF INVENTION: No. 6214348el FtsY
NUKBER OF SEQUENCES: 4
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CLASSIFICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 09/007,484
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Patent No. 6214348
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ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
TELEFAX: 215-994-2222
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US-09-309-682-3
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                                                                                                                                                                                                                                                     Indels 21;
                                                                                                                                                                                                     Length 831;
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APPLICANT: Rosteck Jr., Paul R.
TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
TITLE OF INVENTION: Fisy
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                                                                                                                                                                                                Score 102.4; DB 4;
Pred. No. 6.4e-17;
0; Mismatches 261;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 51.5%;
Matches 300; Conservative (
                     SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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STATE: Indiana
COUNTRY: US
                                                                                                                         ; TOPOLOGY: linear
US-09-309-682-3
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US-08-986-963-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.5%; Score 102.4; DB 2; Length 1278; Best Local Similarity 51.5%; Pred. No. 7.5e-17; Matches 300; Conservative 0; Mismatches 261; Indels 21;
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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Job time : 106 secs
           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/986,963
FILING DATE: December 8, 1997
CLASSIFICATION: 435
ATTORNET/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,72
REFERENCE/DOCKET NUMBER: 31,763
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    LENGTH: 1278 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1278
US-08-986-963-1
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Sequence 8958, Ap Sequence 8030, Ap Sequence 1945, Ap Sequence 1949, Ap Sequence 3764, Ap Sequence 1985, Ap Sequence 1013, Ap Sequence 1, Applisequence 1847, Ap Sequence 116, Ap Sequence 22417, Ap Sequence 22417, Ap Sequence 22417, Ap
                                                                           February 24, 2003, 23:49:06; Search time 75 Seconds (without alignments) 10244.303 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                    US-09-943-108A-1
1368
1 atggcatttgaaggcttatc.....gtatgaatttaccgttttaa 1368
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-815-242-8030

US-09-815-242-4365

US-09-815-242-1369

US-09-815-242-3890

US-09-815-242-3890

US-09-815-242-6164

US-09-815-242-1985

US-09-815-242-1985

US-09-815-242-1985

US-09-815-242-1985

US-09-816-44-7

US-09-816-44-7

US-09-816-44-91

US-09-816-44-91

US-09-816-44-91

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US-09-816-44-91

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US-09-815-242-9991
US-09-815-242-2247
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US-09-790-988-1
                                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                     442118 seqs, 280819700 residues
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                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                  nucleic search, using sw model
                                                                                                                                                                                            Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match Length
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703.4
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463.2
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328.4
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Maximum DB seq
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                                                                                                                                                                  Sequence:
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Perfect
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20 280 20.5 1374 10 US-09-815-242-7850 Sequence 7850, Ap 22 255, Ap 22 2 10 US-09-815-242-3369 Sequence 3369, Ap 22 259 18.6 13.7 10 US-09-815-242-7465 Sequence 7465, Ap 24 160.4 11.7 1440 9 US-09-938-8428-877 Sequence 877, App 25 145.6 10.6 1251 10 US-09-938-8428-877 Sequence 877, App 26 143.2 10.5 939 10 US-09-815-242-8028 Sequence 877, App 27 133 9.7 1329 10 US-09-815-242-8028 Sequence 877, App 27 132 9.7 1329 10 US-09-815-242-6807 Sequence 877, App 27 132 9.7 1329 10 US-09-815-242-6807 Sequence 877, App 27 132 9.7 1329 10 US-09-815-242-6807 Sequence 877, App 27 132 9.7 1329 10 US-09-815-242-6807 Sequence 877, App 28 1102.4 7.5 1278 10 US-09-815-242-9165 Sequence 9165, App 13 102.4 7.5 1278 10 US-09-815-242-9165 Sequence 9165, App 13 102.4 7.5 1278 10 US-09-815-242-9165 Sequence 9165, App 13 102.4 7.5 1278 10 US-09-815-242-9165 Sequence 9165, App 14 1220 10 US-09-815-242-9165 Sequence 917, App 14 1220 10 US-09-815-242-691 Sequence 6201, App 14 1220 10 US-09-815-242-691 Sequence 6201, App 14 12 120 10 US-09-815-242-691 Sequence 1094, App 14 12 120 10 US-09-915-242-691 Sequence 1094, App 14 15.6 4.1 610 9 US-09-915-243-1349 Sequence 1094, App 14 15.6 4.1 610 9 US-09-915-243-1349 Sequence 1094, App 14 15.6 4.1 610 9 US-09-915-245-1349 Sequence 1094, App 14 15.6 4.1 610 9 US-09-915-245-1349 Sequence 1094, App 14 15.2 3.3 819 10 US-09-922-261-185 Sequence 185, App 14 15.2 3.8 819 10 US-09-922-261-185

## ALIGNMENTS

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US-09-815-242-8968
US-09-815-242-8968
Sequence 8968, Application US/09815242
Sequence 8086, Application US/09815242
Sequence 8086, Application US/09815242
Setent No. US20020001569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, Staphylococcus aureus
APPLICATION: (1)...(1368)
US-09-815-242-8968
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GFGAAAAATCTAGGACCACTGGATGATATTATGAAAATGATTCCAGGTATGAATAAATG 1080
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                                                                                1021 GTGAAAATCTAGGACCACTGGATGATATTATGAAAATGATTCCAGGTATGAAAATG
                                                               AAAGGGCTAGATAAGCTTAATATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATC
                                                                                                                              1141 CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACACATTGAATGTATCACGTAAAAAG
                                                                                                                                                                                            CGTATTGCTAAAGGGTCTCGGTCGTTCATTACAAGAAGTCAATCGTTTGATGAAACAATTT
                                                                                                                                                                                                                          1201 CGTATTGCTAAAGGGTCTCGTTCATTACAAGAAGTCAATCGTTTGATGAAACTATT
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Pred. No. 2e-284;
0; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE:
PRIOR APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR PLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PLILAGATION NUMBER: 60/242,578
PRIOR PLILAGATION NUMBER: 60/242,578
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 8030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Undith W.
APPLICANT: Zyskind, Undith W.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Ess
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8030, Application US/09815242 Patent No. US20020061569A1
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98.9%;
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APPLICANT: Haselbeck, Robert
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Best Local Similarity 98.9°
Matches 1353; Conservative
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US-09-815-242-8030
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                                                                                                                                              GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT 120
                                                                                                                                                                             GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTACTT 120
                                                Gaps
                                                                                                      1 AFGCCATTTGAAGGGTTATCAGAACGCTTGCAAGGGACGACGATGCAAAAAAATGCGTGGTAAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGTTAAGTTTAATTGAAAAAGCGCAACAAGATGTGGGATCAAGAAAAAGCAAAAAGATTTA
                                                                                1 ATGGCATTTGAAGGCTTATCAGAACGCCTGCAAGCGACGATGCAAAAAATGCGTGGTAAG
                                                                                                                                                                                                             TTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATAGTTCAA
                                                                                                                                                                                                                                                                                                                                         GATGAATTAACGAAGTTGATGGGTGGAAAAATACATCGATTAATATGTCAAATAAACCA
                                                                                                                                                                                                                                                                                                                                                             TACAGTGAAGGAGATCAAGTAAAGCCACAAAATTGTAACTAATGCATTAAAACATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGAAGAACATTTAGACTTTGTAATCATTGATACAGGCGGGTCGATTACACATGGAA
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0
                                                Indels
                DB 10;
             Score 1356.8; DB 1:
Pred. No. 3.2e-287;
0; Mismatches 7;
             99.28;
                                                Conservative
                               Similarity
                                             Matches 1361;
                Query Match
                                   Local
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FILE REPERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: 05/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FESTEREQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                        CGCAATCAAATGCAAAATATGTTAAAAGGTATGAATTTACCGTTTTAA 1368
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US-09-815-242-4365
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Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Haselbeck,
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Yu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
FITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELLTRA.011A
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99.2%; Pred. No. 1.1e-144;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 05/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2001-02-16
PRIOR PLILING DATE: 2001-02-10-07
PRIOR PLILING DATE: 2001-02-10-07
PRIOR PLILING DATE: 2001-02-10-07
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Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haselbeck, Robert
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Matches 707; Conserv
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US-09-815-242-1949/c
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FILE REFERENCE: ELITRA.011A
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-03-21
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PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
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Patent No. US20020061569A1
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T: Zyskind, Judith W.
T: Wall, Daniel
T: Trawkick, John D.
T: Carr, Grant J.
T: Yamamoto, Robert T.
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US-09-815-242-3890
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Best Local Similarity 64.8
Matches 844; Conservative
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                                                                                               1141 CTATCAATGACCCCTGCAGAACGTGAAAATCCTGATCTATTAAATCCTAGTCGCGTCGC
                                    CCTGGTATTGAAAATGTCAAAGTCGATCCAAAAGATGTGGCACGGAAACGGGCGATGGTC
                                                                         CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACACATTGAATGTATCACGTAAAAAG
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64.8%; Pred. No. 3.4e-115;
tive 0; Mismatches 459; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US,09/815,242
                                                                                                                                                                                                                         1261 AACGATATGAAGAAATGATGAACAATTCACTGGTGGCGGTA 1303
                                                                                                                                                                                                                                                            1261 AAAGAATCCAAAAAATGATGCAACAAATGTCCAAAGGGGATA 1303
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Patent No. US20020061569A1
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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APPLICANT: Haselbeck, Robert
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Matches 844; Conservative
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                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
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1201 AGAATIGCAGCIGGIICAGGAAAIAGIGIGGIIGAAGICAAICGIAIGAIIAAACAAITI 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATAGTTCAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                       AACGATATGAAGAAAATGATGAAACAATTCACTGGTGGCGGTA 1303
                                                                461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.3%; Score 565; DB 10; 64.5%; Pred. No. 3.2e-114;
                                                                                                                                                                                                                                                                                                                                                           Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/046,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                             Sequence 37, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (301) 309-8504
(301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome
STREET: 9410 Key West Av
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 6729 base pairs
                                                                                                                                                                                                                                       APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                Steven Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland COUNTRY: USA
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                                                                                                                                        RESULT 7
US-09-070-927A-37
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59 AGGGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTAT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATTAGGTICCGAIGTAATGCAATCATTAACACCAGGGCAACAAGTATTAAAATAGTIC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAAAATAGTTC 238
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161 TITATCGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTG 102
                                                479 TATACAGTGAAGGAGATCAAGTAAAGCCACAACAAATTGTAACTAATGCATTAAAACATG
                                                                                               101 TATACAGTGAAGGAGATCAAGTAAAGCCACAACAATTGTAACTAATGCATTAAAACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                539 CTAAAGAAGAACATTTAGACTTTGTAATCATTGATACAGCA 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                       41 CTAAAGAAGAACATTAGACTTTGTAATCATTGATACAGCA 1
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Pred. No. 7.1e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRICR APPLICATION NUMBER: 60/191,078
PRICR FILING DATE: 2000-03-21
PRICR FILING DATE: 2000-03-21
PRICR FILING DATE: 2000-05-23
PRICR FILING DATE: 2000-05-23
PRICR FILING DATE: 2000-05-26
PRICR FILING DATE: 2000-05-26
PRICR FILING DATE: 2000-05-36
PRICR FILING DATE: 2000-11-27
PRICR FILING DATE: 2000-11-27
PRICR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 2013 LENGTH: 521
                                                                                                                                                                                                                                                                                                                        Sequence 2013, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
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99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert
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Best Local Similarity 99.4
Matches 518; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCTACTGTTGTTATGATGGTTGGTTTACAAGGTGCTGGTAAAACAACACTGCAGGTA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     521 AGGGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTAC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 TTGAGGCTGACGTAAACTTTAAAGTGGTAAAAGAATTTATTAAAACAGTATCAGAACGCG 402
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                                                                                                                                                                                                                                                                 APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Proxaryotes
4982 AAAGAATCCAAAAAATGATGCAACAAATGTCCAAAGGGGATA 5024
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                    Sequence 1985, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Staphylococcus aureus
US-09-815-242-1985
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ilarity 99.4%;
Conservative
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Zyskind, Judith W.
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Matches 518; Conserv
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                                                                        RESULT 8
US-09-815-242-1985/c
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APPLICANT:
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                                         CACCTACTGTTGTTGATGGTTGGTTTACAAGGTGCTGGTAAAACAACAACTGCAGGTA
                                                                              TTTATCGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTG
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                 36.3%; Score 496; DB 10;
61.1%; Pred. No. 2.4e-99;
live 0; Mismatches 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
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PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-3
PRIOR PLING DATE: 2000-05-3
PRIOR PILING DATE: 2000-05-3
PRIOR PILING DATE: 2000-05-3
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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SOFTWARE: FastSEQ for Windows Version
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PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR FILING DATE: 2001-02-16
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APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xamanoto, Robert T.
APPLICANT: Xu, H. Howard
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Zyskind, Judith W.
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US-09-815-242-9427
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SOFTWARE: FASTOR
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US-09-815-242-9427
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                                                           GCATTGATGAACGAATTAAAAAGAAGTAAAAGAAATTGCTAAAACCAAACGAAATTATGTTA
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APPLICANT: Haselbeck, Robert
APPLICANT: Aselbeck, Robert
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essent;
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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Patent No. US20020061569A1
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APPLICANT: CHEEVER, CHRISTY
APPLICANT: TECTRAU, DOUGLAS A.
APPLICANT: TECTRAU, DOUGLAS A.
APPLICANT: TECTRAU, DOUGLAS A.
APPLICANT: TANNE, DAVID J.
APPLICANT: PANG, LEI
TILE OF INVENTION: AND POLYPEPTIDES COMPOUNDS MODULATING THEIR ACTIVITY
FILE REPERENCE: 6850069
TITLE OF INVENTION: MANGER: US/09/814,041A
CURRENT APPLICATION NUMBER: 150103-20
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 2
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 2.5e-99;
0; Mismatches 510; Indels 0
                                                                                                                                                                                            Sequence 1, Application US/09814041A Patent No. US20020103104A1
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61.1%;
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Matches 730; Conservative C
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US-09-974-300-1847
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ilarity 61.1%; Pred. No. 2.5e-99;
Conservative 0; Mismatches 510;
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SOFTWARE: FastSEQ for Windows Version 4.0
                        PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-02-3
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
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60/191,078
                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Streptococcus pneumoniae
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US-09-815-242-9156
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SERVISAL INPORATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Repression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT APPLICATION NUMBER: US/09/974,300
FILE REPRESSION NUMBER: 09/680,598
FRIOR PILING DATE: 2001-10-06
FRIOR FILING DATE: 2000-10-06
FRIOR FILING DATE: 2001-06
FRIOR PILING DATE: 2001-06
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FRIOR FILING DATE: 2001-06
FRIOR FILING DATE: 2001-06
FRIOR SEPTING DATE: 2001-06
FRIOR FILING DATE: 2001-06
FRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 8481 Indels Score 486.4; DB 10; Pred. No. 2.8e-97; 0; Mismatches 406; ; Sequence 1847, Application US/09974300 ; Patent No. US20020146721A1 Bacillus licheniformis

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larity 99.4%; Pred. No. 2.6e-92;
Conservative 0; Mismatches 3;
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FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/191 078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                        APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
                                                                                                             Sequence 3070, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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                                                                                                                                                                                        Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                   APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                        Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: ELITRA.011A
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                                                                                                                                                                                                                                          CCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTATACAGT 486
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                   CAAATTGATATTCCTGTATACAGTGAAGGAGATCAAGTAAAGCCACAAAATTGTAACT 49
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                                                                     AATGCATTAAAACATGCTAAAGAAGAACATTTAGACTTTGTAATCATT 570
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TITLE OF INVENTION: Identification of Essent:
TITLE OF INVENTION: Identification of Essent:
TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT ELING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/201,08
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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SOFTWARE: FastSEQ for Windows Version
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Patent No. US20020061569A1
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ORGANISM: Haemophilus influenzae
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. HAMMANDER
                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Best Local Similarity 59.2
Matches 775; Conservative
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AZ529841 AY109321 BQ996389 AW930742 AZ682189 BH147501 AK011928

A1087737 BH369841

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AW930742 EST356585 AZ682189 ENTKB30TF BH47501 ENTQALBTF BH47501 ENTQALBTF BH37501 ENTQALBTF BH37573 SWANCAC23 BH325805 PICL\_53\_A AV106667 Zea mays BES96266 PIL\_51\_F0 AW049149 EST327603 A43727 T3 end of B1512818 BB16010A AW147928 Ga29406.X B17454259 GGG1A010A AW147928 Ga29406.X B1745259 GGG1A010A BP33657 EST459627 BG317280 947027511 BG98609 GGGLAOU.

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        GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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BM325805 A7106667 BES6865 AW033339 AW0423339 CNG07B07 B1512818 BQ73695 B1512818 BQ73695 B154259 BP736572 BP736572 BP736572 BP73698 BP74133 BP74133 BP74133 BP74133 BP74133 BP74144444

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ALIGNMENTS

BE461473

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LIMGtag644 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, DNA sequence.
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                                                                                                                                                  Lactococcus lactis subsp. cremoris.
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                         Dolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments, (2002) In press
Contact: Sorokin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: shotgun
High quality sequence start: 30
High quality sequence stop: 2141.
Location/Qualifiers
1. 2169
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCAAACGAAATTATGTTAGTTGTCGATTCAATGACGGGTCAAGATGCTGTCAATGTTGC 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAAATTGATATTCCTGTATACAGTGAAGGAGATCAAGTAAAGCCACAAAAATTGTAAC 521
                                                                                                                                                                                                                                              225 TATTAAAATAGITCAAGAIGAAITAACGAAGITGAIGGGIGGAGAAAAIACAICGAITAA 284
                               /db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="vector: pSGMU2; Site_1: Smal; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial Alul digestion or by sonication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAACTIGACATICCIGITTAIGAIGAAGGAACGICTGAAAAACCCGTIAATAITGICCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCAACAGAAATTTTACTCGTTGTTGATGGGATGACTGGTCAAGTGGCCGCACAAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAATCTTTTGACGATCAACTTGATGTCACAGGTGTTACCTTAACTAAATTAGATGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           822 IGGIAIGAGIGAAAAGIIAGAIGGIIIAGAGCIAIICCAICCIGAACGIAIGGCAICACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGGACTGGTGAAAAATTAACCGACCTTGAAGTTTTCTACCCTGATGGTATGAGCTCAAG
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   cremoris
                                                                                                                                                                          Length 2169;
                                                                                                                                                                                                         0; Mismatches 390; Indels
'organism="Lactococcus lactis subsp.
                                                                                                                                                                        Score 422; DB 17;
Pred. No. 1.4e-80;
                  /strain="MG1363"
                                                                                                                                                                        30.8%;
63.7%;
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                            Similarity
                                                                                                                        642
                                                                                                                                                                                                           Matches 689;
                                                                                                                                                                          Query Match
                                                                                                                                                                                              Best Local
                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1929
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//clone="crobising"
//clone=lib="tomato flower, anthesis"
/tissue_type="flower"
/tissue_type="flower"
/dev_stage="anthesis"
/dev_sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST54107 tomato flower, anthesis Lycopersicon esculentum cDNA clone cT0D18716 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum Bukaryota, Firidiplantee, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridee; euasterids 1; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J., Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue, anthesis (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleanson University
100 Jordan Hall, Clemson, SC 29634, USA
110 Jordan Hall, Clemson, Sc 29634, USA
1115 clone is available through the Clemson University Genomics
Institute
                                         GAATGTATCACGTAAAAAGCGTATTGCTAAAGGGTCTGGTCGTTCATTACAAGAAGTCAA 1241
                                                                                                                                                                                                             1209 AFCGCCAGCTCGTCGTCGTCGAFCGCCGCAGGTFCTGGGAAFFCAFFTAFTGAAGFAAA 1150
                                                                                                                                                                                                                                                                                     TCGTTTGATGAAACAATTTAACGATATGAAGAAATGATGAAACAATTCACTGGTGGCGG 1301
1122 TCATATTAAAGCGATTATCCAGTCAATGACGCCGGCTGAAAGAAGAACAATCCAGACACATT 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 TAITTGAGGCTGACGTAAACTTTAAAGTGGTAAAAGAATTTATTAAAACAGTATCAGAAC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 GCGCATTAGGTTCCGATGTAATGCAATCATTAACACCCAGGGCAACAAGTTATTAAAATAG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 2.5e-43;
0; Mismatches 319; Indels
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/cultivar="TA496"
/db_xref="taxon:4081"
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1, .773
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Best Local Similarity 58.5%;
Matches 453; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
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DEFINITION
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ORGANISM
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JOURNAL
COMMENT
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KEYWORDS
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5'-dacradifications and analytical lines are selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                /note="Wector: pCMV-SPORT6 (Life Technologies); Site_1: OBMI; Site_2: Sall; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-ICGACCCACGCGCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAAAGATGCGTGAGTCATCGTTTACTTTAGATGATTTTTTAGAACAACTTGATCAGGT 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGCTAGA-TAAGCTTAATATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATCC 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1142 AGTCAATGACGCCGGCTGAAAGAAACAATCC-----AGACACATTGAATGTATCACGTA 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     903 GTTAAGTTTAATTGAAAAAGCGCAACAAGATGTGGATCAAGAAAAAGCAAAAGATTTAGA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 TTGAAGGCATTGATTTTTCTCAAGGAGAAAACAAATGGCTACAGTTAAAGCAATCATAC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604 ITGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAACCAAACGAAATTATGTTAGTT 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCGATTCAATGACGGGTCAAGATGCTGTCAATGTTGCAGAATCTTTTGACGATCAACTT 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITCAATAAGAGACATTACTGGCAAGCCAATTAAATTTGTTGGTGTTGGTGAACAGATGAG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGTCACAG-GTGTTACCTTAACTAAATTAGATGGTGATACACGTGGTGGTGCAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCIATTCGTTCGGTGACACAAAAACCAATTAAATTTGTTGGTATGAGTGAAAAGTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 CCTTCTTTAATAGAAAAGCTCAGCAAGCTATTGACCAAGATGAAGTAAAGTTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAAAATCTAGGACCACTGGATGATATTATGAAAATGATTCCAGGTATGAATAAAATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCTTTCAGNGAATAATATTAACAAAGTTAGATGGTGATACAAGAGGTGGTGCTGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:3280811"
/clone=lib="Lupski_dorsal_root_ganglion"
/sax="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAGCGTATTGCTAAAGGGTCTGGTCGTTCATTACAAGAAGTCAA 1241
    found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                     /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 243.8; DB 1
Pred. No. 2.7e-42;
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                                                               433.
                       info@image.llnl.gov
Seg primer: -400P from Gibco
High quality sequence stop: 4
Location/Qualifiers
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Emal: gqapbs-rémail.nih.gov
Tissue Procurement: Dr. James Lupski
CDNA Library Preparation: Lupski Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7d99a06.x1 Lupski_dorsal_root_ganglion Homo sapiens CDNA clone IMAGE:3280811 3' similar to SW:SR54_BACSU P37105 SIGNAL RECOGNITION PARTICLE PROTEIN; mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 711)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AAGCCGTTGGCACTGGTTTGATTCGAGGTGTAAAACCAGATCAGCAACTAGTTAAGACTG 121
                                                                                                                                                                                                                                                                                                   416 ATATTTATCGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTC 475
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TACGTGACGAGCTTTTTGTAAAT
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Triticum aestivum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
I (bases I to 656)
SA Altenbach, S., Anderson, C.D., Chao, S., Chin, A., Close, T.J., Cronin, K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J.,
Wilson, C. and Woo, J.
Wilson, C. and Woo, J.
The structure and function of the expressed portion of the wheat
genomes - Developing grains cDNA library
Upphilshed (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 31-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHE3566_H12_P242S Wheat developing grains cDNA library Triticum eastivum cDNA clone WHE3566_H12_P24, mRNA sequence. BQ805434 BQ805434 I GI:22029643
                                                                                                                                                                                                                                                                                                                                                    ATTTAGAG --- AAAAAGATGCGTGAGTCATCGTTTACTTTAGATGATTTTTAGAACAAC 1012
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                                                                                                                                                                               291 AAACCGACGCGCTGGAGCCATTCCATCCGGATCGTATCGCCTCGCGTATTCTCGGCATGG 232
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     411 AAGCGCTGCCGTTAACCGGCGTGGTGCTGACCAAAGTTGATGGTGATGCGCGTGGCGGTG 352
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                                                      CAGCTTTATCTATCGTTCGGTGACACAAAAACCAATTAAATTTGTTGGTATGAGTGAAA
                                                                                 836 AGTTAGATGGTTTAGAGCTATTCCATCCTGAACGTATGGCATCACGTATTTTAGGTATG
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/clone_lib="Wheat developing grains cDNA library"
/tissue_type="Whole grains"
/dw_stage="1-44 days post anthesis seed"
/lab_host="E. coli SoLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GGCAGATICCGGACAACGTIAAATCGCAGATGGATGACAAG 11
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/cultivar="Butte 86"
/db_xref="taxon:4565"
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                                                                                                                        AF075878 Salmonella typhimurium LT2, Lambda DASH II Salmonella typhimurium genomic clone 245-T3, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                              Wong, R.M.-T., Wong, K.K., Benson, N.R. and McClelland, M. Sample sequencing of a Salmonella typhimurium LT2 lambda library: comparison to the Escherichia coli K12 genome consarison to the Escherichia coli K12 genome PENKS Microbiol. Lett. 173 (2), 411-423 (1999)
                                                                                                                                                                                                                                                                     Salmonella typhimurium.
Salmonella typhimurium
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Salmonella typhimurium LT2, Lambda DASH II"
/note="Vector: Lambda DASH II; sequenced using Li-Cor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 GTAAATTAGCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGCAGCAG 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAAGCATTGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAAACCAAACGAAATTA 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17; Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 232.2; DB 17; Length
Pred. No. 8.4e-40;
0; Mismatches 358; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA 92121, USA
108 AGAGAAGAATAGCIAAAGGTICIGGIACAACAGIACAAGAAGNIAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Salmonella typhimurium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular Biology
Sidney Kinnel Cancer Center
3099 Science Park Road, San Diego,
Email: mcclelland@lifsci.sdsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="LT2"
/db_xref="taxon:602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="245-T3"
                                                                                                                                                                                                                         AF075878.1 GI:3320748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: McClelland M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.0%;
                                                                                                                                                                                                                                                                                                                                                 Salmonella.
1 (bases 1 to 875)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 56.0
Matches 460; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: shotgun.
                                                                                                                                                                                                    AF075878
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                                                                           RESULT 4
AF075878/c
                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531
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COMMENT
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                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                         VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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1 (bases 1 to 593)
Alcala,J., Varbalov,J., White,R., van der Hoeven,R.S, Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Glovannoni,J.J., Martin,G.B. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="romato germinating seedlings, TAMU"
/tissue_type="whole seedlings"
/dev_stage="/ days post imbiblition"
/note="vector: pBlueScript SK(-); Site_1: EcoR1: Site_2:
Xhol; 7 days post imbiblition on water-agar. Mixed stage
whole germinating seedlings from seed coat emergence up
to two centimeters in seeds not showing obvious signs of
germination were discarded."
                                                                                                                                                                                                                                                                                                          Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 GACGIGAAACGGGIACTGAACCCCACAGAGGITITACITGITGIGGATGCAATGACTGGC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGATGCTGTCAATGTTGCAGAATCTTTTGACGATCAACTTGATGTCACAGGTGTTACC 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 CAATTACAAACAGTAGGGAAACAAATTGATATTCCTGTATACAGTGAAGGAGGATCAAGTA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 AAGCCACAACAATTGTAACTAATGCATTAAAACATGCTAAAGAAGAACATTTAGACTTT 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CAACTIGITATITIGGGTAAAACAGGTIGATGTACCIGTITATGCAGGAACAGATGTA 61
                                                                                                                                                                                                                                                                              Lycopersicon esculentum
Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheol
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTAATCATTGATACAGCAGGTCGATTACACCATGAAGCATTGATGAACGAATTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGTAAAAGAAATTGCTAAACCAAACGAAATTATGTTAGTTGTCGATTCAATGACGGGT
                                                                                       AW648731 593 bp mRNA linear EST 11 EST327101 tomato germinating seedlings, TAMU Lycopersicon esculentum cDNA clone cLEI5G22 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute clemson University 100 Jordan Hall, Clemson, SC 29634, USA Enail: http://www.genome.clemson.edu/orders/index.html prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 218; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generation of ESTs from germinating tomato seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .593
/organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 221.2; DB 1 Pred. No. 1.9e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4081"
/clone="cLE15G22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon
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                                                                                                                                                                                                                                                          tomato.
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KEYWORDS
SOURCE
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                                    RESULT 6
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Environment 3) 370C/170C day/night, well-watered, with post-anthesis fertilizer. Environment 4) 370C/170C day/night, well-watered, without post-anthesis fertilizer, Environment 4) 370C/170C day/night plus drought, without post-anthesis fertilizer, day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Altenbach and R. Cronin at USDA-ARS, Albany, CA. A CONRA library was made using poly (A) RRA, and the CDNA clones were in vivo excised to give pBluescript SK(-) phagemids in the TJ Close Lab (Chlin, Close, Fenton) at the Day Environment 2 of 24, 28, 28, 29, 29, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20, 24, 28, 30, 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGAAAAGAAATAATATTGATGCGATCGTAGTGGATACTGCTGGCAGACTGCAGATTGATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     719 AACTIGATGTCACAGGTGTTACCTTAACTAAATTAGATGGTGATACACGTGGTGGTGCTGCTGCTG 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           779 CITIAICIATICGATCGGTGACACAAAAACCAATTAAATTIGTIGGTAIGAGTGAAAGT 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 IGGAGGACCTIGAGCTITICTATCCCGACCGCATGGCACAACGIGTTTTGGGAATGGGAG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 TTTATCGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGATATTCCTG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 TATACAGTGAAGGAGATCAAGTAAAGCCACAACAAATTGTAACTAATGCATTAAAACATG 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              599 AAGCATTGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAACCAAACGAAATTATGT 658
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preparations and DNA sequencing were performed
Anderson lab (others)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 656;
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1 (bases I to 677)
Alcala, T. Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai, J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of ESTs from tomato fruit tissue, breaker stage (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 22-JAN-2002
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
    179 AAATTAGCAAACTTCCTGAAGAAAAAGAGCAAAAATCCGTTATTGGTAGCATGTGAC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 TGAAGCATTGATGAACGAATTAAAAGAAGTAAAAGAAATTGCTAAACCAAACGAAATTAT 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 TGAAGAGATGATGAACGAAATTCGTAACGTTCACCAGTCTGTAAAACCTACAGAAACTCT 478
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/cultivar="TA496"
/db_xref="taxon:4081"
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Contact: CUGI
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001) Other_GSSS: AG-ND-138B11.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This close is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from naxed seekes of larvae. The BAC library was constructed at Texas AAM University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partition and Misseless of the Station of DNA is a feature of the BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                               421
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802 CAAAAACCAATTAAATTTGTTGGTATGAGTGAAAGTTAGATGGTTTAGAGCTATTCCAT 861
                                                                                                                                                                                                  238 CAAGATGAATTAACGAAGTTGATGGGTGGAGAAATACATCGATTAATATGTCAAATAAA 297
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                           AGAAAGCCAATCAAGCTGGTGAAGGGGTGAAGGAGGTGTTGGAGGACCTTGAAT
                                                                                                              2 GCTTTAGGACAAATGTTTAACATCCATTACCCCGGGACAATTGATGACAAAATTGTT
                                                                                      CCTGAACGTATGGCATCACGTATTTTAGGTATGGGTGATGTGTTTAAGTTTAAAAAA
                                                                                                                                                                       GCGCAACAAGAIGIGGAICAAGAAAAAGCAAAAGAITIAGAGAAAAAAAIGCGIGAGICA
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryç
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Pred. No. 1.4e-36;
); Mismatches 223; Indels
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The Institute for Genomic Research
9712 Medical Corter Dr., Rockville, MD 20850, USA
Fax: 301 838 3543
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193 t
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                                                                                                                                                                                                                                                             TCGTTTACTTTAGATGATTTTTTAGAACAA 1011
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/clone_lib="ND-TAM"
/note="Vector: pECBAC1;
118 c 154 g 19
                                                                                                                                                                                                                                                                                      542 AAATTGATTGCAATGACTTCCTGAAGCAA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="PEST"
/db_xref="taxon:7165"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bjloftus@tigr.org
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Seq primer: M13 For
Class: BAC ends.
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Alcala, T. Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tankeley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: Xho1; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 TATGATGGTTGGTTTACAAGGTGCTGGTAAAACAACAACTGCAGGTAAATTAGCATTATT 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 1GCTATTGACCAACTTGTTATTTTGGGTAAACAGGTTGATGTACCTGTTTATGCAGGG
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                                                                                                                   Generation of ESTs from tomato fruit tissue, breaker stage
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س
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.9%; Score 190.6; DB 10; Length 605; llarity 58.6%; Pred. No. 7.3e-31; Conservative 0; Mismatches 244; Indels 3;
                                                                                                                                                                                                                             100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
                                                                                                                                                                                                                                                                                                                                                      esculentum'
                                                                                                                                                                                         Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                 /organism="Lycopersicon/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4081"
/clone="clEG7M2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                            Clemson University
                                                                                                                                           (2000)
                                                                                                                                                                                                                                                                                                                         1. .605
                                                                                                                                           Unpublished (Contact: CUGI
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Matches 35
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                                                                                                            Site_2: XDOI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
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Bukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanacee; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 AGTGGGGGAACAGGTTGATGTACCTGTTTATGCAGCAGGAACAGATGTAAAACCTGCAGA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAGCCCGACAAGGATTACAAGAGGCCCAAAAGAAGAATGTAGATGTAGTCATAATGGA 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633 AATIGCIAAACCAAACGAAATIAIGTTAGTIGTCGATICAAIGACGGGTCAAGGIGCTGT 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 GGTACTGAACCCCACAGAGGTTTTACTTGTTGTGGATGCAATGACTGGCCAAGAAGCTGC 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 AGCTTTGGTCACAACATTCAATCTCGAAATTGGAATTACTGGTGCCATCTTGACGAAGCT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    813 TAAATTTGTTGGTATGAGTGAAAAGTTAGATGGTTTAGAGCTATTCCATCCTGAACGTAT 872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 GTATGCGTCAAGAAGATGCTGAAGAATTGCAGAAGAAGATCATGAGTGCAAAATTTGATT 630
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                              /note="Vector: pBluescriptSXmCUadapt; Site_1: EcoR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                              Score 210.4; DB 13; Length 677;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.1e-35;
0; Mismatches 211;
/clone_lib="tomato breaker fruit"
                          /tissue_type="Pericarp"
                                             /dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone cLEG7M2, mRNA sequence
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62.1%;
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Matches 348; Conservative
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496035E06.x1 496 - Stressed shoot CDNA library from Wang/Bohnert
lab Zea mays CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            996 IGATITITIAGAACAACTIGATCAGGIGAAAAATCIAGGACCACIGGAIGAIATIAIGAA 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 GCGCAAGAAGAGGCTGTAGAATTACAGAAAAAGATCATGAGTGCAAAATTCGACTTCAA 425
                                                                                                                                                                                                                                                                                                                                                                                                                     306 ACAGCGAGTATTGGGAATGGGAGATGTACTCTCATTTGTTGAAAAGACACAAGAAGTTAT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 CGACTTCTTAAAACAATCTCAAAATGTTGCGAAAATGGGTTCCATGAGCCGCATTATTGG 485
     66 TGTTAATCCTACAGAAGTTCTGCTTGTCGTTGATGCCATGACTGGCCAAGAAGCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       936 GGATCAAGAAAAGCAAAAGATTTAGAGAAAAAGATGCGTGAGTCATCGTTTACTTTAGA 995
                                                                                                                               126 ACTAGTCACCACCTTCAATATTGAGATTGGTATCACTGGTGCTATATTGACTAAATTGGA 185
                                                                                                                                                                                 186 TGGTGACTCCAGGGGGGGGAGCCGCACTAAGTGTTAAAGAGGTCTCTGGGAAGCCCATCAA 245
                                                                                                                                                                                                                                                                                   816 ATTICITGGTATGAGAGAGATTAGATGGTTTAGAGCTATTCCATCCTGAACGTATGGC 875
                                                                                                                                                                                                                                                                                                                                                                                        876 AICACGIATITIAGGIAIGGGIGAIGIGITAAGIITYAATIGAAAAAGCGCAACAAGAIGI 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="salt stress"
/lab_host="E.coli XL Gold"
/note="Organ: shoot; Vector: pBluescriptII SK(+) XR;
Wang/Bohnert"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cultivar="B73" "-1
/db_xref="taxon:4577"
/clone_lib="496 - stressed shoot cDNA library from
Wang/Bohnert lab"
/tissue_type="seedling"
                                                                                  696 IGTTGCAGAATCTTTTGACGATCAACTTGATGTCACAGGTGTTACCTTAACTAAATTAGA
                                                                                                                                                                                                                                                                                                              1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                855 California Ave, Palo Alto, CA 94304, USA
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Plate: 496035 row: E column
Location/Qualifiers
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Walbot, V.
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Unpublished (1999)
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Fax: 650 725 8221
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/dev_stage="4-week-old seedlings infected with
Collectorichum graminicola"
/dote="vyector: pBluescript II SK(-) from Lambda Zap II;
Site_1: XhoI; Site_2: EcoRI; Four-week-old sorghum
seedlings were sprayed with spore suspension prepared from
3-week-old FRMAI, a sorghum isolate of the anthracnose
pathogen Colletorichum graminicola. Incculated plants
were kept in a 25 cark growth chamber with 100% relative
humidity for 24 hr. followed by 12/12 hr of light/dark
cycle at 25 c with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTS are expected to derive
from the host plant, no effort was made to eliminate ESTS
deriving from the pathogen."
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                                                                                                                                                       BM323434 1514 bp mRNA linear EST 04-JAN-2002 PICL_19_C04.bl_A002 Pathogen-infected compatible 1 (PICL) Sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
Sequences have been trimmed to exclude Polyh, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20. Three-prime sequences, which are obtained with Polyymix or
T7 sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 454
POLYFANO.
                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACC clade, Panicoldeae, Andropogoneae, Sorghum.

    Chases 1 to 514)

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An EST database from Sorghum: plants infected with a compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
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/db_xref="taxon:4558"
/clone_lib="Pathogen-infected compatible 1 (PIC1)"
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Pred. No. 3.2e-30;
0; Mismatches 199; Indels
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                                                                                                                                                                                                         bicolor cDNA, mRNA sequence.
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/strain="HM1:IMSS"
/db_xref="taxon:5759"
/db_xref="taxon:5759"
/cloe_lil="Entamoeba histolytica Sheared DNA"
/cloe_lil="Entamoeba histolytica Sheared DNA"
/note="Vector: pHGS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of B. histolytica using a method described by Clark and Diamond (Clark, using a method described by Clark and Diamond (Clark, and Diamond Clark)
                                                                                                                                                                                                                                                                   G.G., and Dismond, L.S. (1993) Entanceba histolytics: method for isolate identification. Exp. Parasitol.

7.450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Maring small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing. A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 TGAATGCTAAACGAGCAGGAGTACCATTTTTGGAATAAAAGAAGAAGAAGTGGTCCAGTAA 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 183.4; DB 17; Length 814;
Pred. No. 2.6e-29;
0; Mismatches 316; Indels 0;
                                                                             /organism="Entamoeba histolytica
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  High quality sequence stop: 811. 
Location/Qualifiers
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illarity 54.1%;
Conservative (
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1 (bases 1 to 814)

Loftus, E., van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTCCTGTATACAGTGAAGGAGATCAAGTAAAGCCACAACAAATTGTAACTAATGCATT 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 AGAACGCGCATTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAAGTTATTAA 230
                                                                                                                                                                                                                               63 TGAAAAGGCTGTAGGCACCGATGTGATCCGAGGTGTCCGACCTGACCAGCAGTTGGTGAA 122
                                                                                                                                                                                                                                                                                               231 AATAGTICAAGAIGAATTAACGAAGTIGAIGGGIGGAGAAAAIACAICGAITAAIATGIC 290
                                                                                                                                                                                                                                                                                                                                           123 GGTTGTGAGGAACTGGTACAACTGATGGGCGGGGGGGGTATCAGATTTGGTGTTTGC 182
                                                                                                                                                                                                                                                                                                                                                                                              AAATAAACCACCTACTGTTGTTATGATGGTTGGTTTACAAGGTGCTGGTAAAACAACAAC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                          183 AAAATCIGGGCCAACTATIATATITTIGGCAGGICTGCAAGGIGTIGGAAAAACTACIGT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCAGGTAAATTAGCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGC 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 AGCAGATATITATCGTCCAGCAGCGATAAATCAATTACAAACAGTAGGGAAACAAATTGA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 AGCGTTATTTGAGGCTGACGTAAACTTTAAAGTGGGTAAAAGAATTTATTAAAACAGTATC 170
                                                   Gaps
                                                                                                                                               3 AGCACTTTTGGAGGCCGATGTAAGTTTGCCAGTAAGAAGATTTATTGAGTCTGTAAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 GAAGGAGGCAAAAGTCAATAAAGCTGATGTAATTATATGTGGACACGGCTGGAAGACTGCA
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Length 581;
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 3543
Fax: 301 838 2543
Email: bjloftusetigr.org
                                                Indels
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6
                                                0; Mismatches 237;
Score 186,4; DB 9
Pred. No. 5.8e-30;
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Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from
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13.6%;
58.7%;
                                                Conservative
                         Similarity
                         Best_Local Sim
Matches 341;
Query Match
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QGG12L07.yg.abl QC_EFGHJ lettuce serriola Lactuca sativa cDNA clone QGG12L07, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabadyh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Separate cDNRs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNR. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNR and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB-GG_ERGHJ lettuce serriola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: akozikeatgo.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig5305, see http://cgpdb.ucdavis.edu/
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/hote="Vector: pBRcDNASflAB; The library was constructed
/note="Vector: pBRcDNASflAB; The library was constructed
from 10 different sources of RNA from a single genotype.
                                                                                                                                                                                                                                                             1162 AGAAACAATCCAGACACATTGAATGTATCACGTAAAAGCGGTATT-----GCTAAAGGG 1215
                                                          1042 GATGATATTATGAAAATGATTCCAGGTATGAATAAAATGAAAGGGCTAGATAAGCTTAAT 1101
                                                                                                                                                              1102 ATGAGTGAAAAGCAAATTGATCATATTAAAGCGATTATCCAGTCAATGACGCCGGCTGAA 1161
                                                                                                                                                                                                                                                                                                                                                                 TOTGGTCGTTCATTACAAGAAGTCAATCGTTTGAAGAACAATTTAACGATATGAAGAAA 1275
     371 AAATTCGACTTCAACGATTTCTTAAAACAATCTCAAAACGTTGCGAAAATGGGTTCCATG 430
                                                                                                                                                                                              --AGCTGAGAAAAGACTTGCATTCGTGGAGTCAATGATGATGCCATGACTGCTGAGGAA 547
                                                                                                                                                                                                                                                                                                               548 AGGGAGAAGCCAGAGTTACTGGCTGAATCACGTGAGGAGGATAAGAGTGGCTGAGGAG 607
                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGGAAAGACTGAACAAGAGGTGAGTCAATTGGTTGCCCAGCTTTTCCAAATGCGTGCT 667
                                                                                                            431 AGCCGCATTATTGGAATGATGCCAGGCATGAACAAGATAACTCCCGCACAAATCCGAGA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Mistandson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
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for details.
Plate: QGG12 row: L column: 07.
Location/Qualifiers
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/db_xref="taxon:4236"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote—"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project " 317 g 279 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGTTTACTTTAGATGATTTTTTAGAACAACTTGATCAGGTGAAAAATCTAGGACCACTG 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 CAAGAAGCAGCACCACTAGTCACCTTCAATATTGAGATTGGTATAACTGGTGCAATA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           802 CAAAAACCAATTAAATTTGTTGGTATGAGTGAAAAGTTAGATGGTTTAGAGCTATTCCAT 861
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Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
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                                                                                                                                   mRNA
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/db_xref="taxon:4577"
                                                                                                                            AY109321 1200 bp
Zea mays PC0070230 mRNA sequence.
AX109321 G::21212876
692 TGCAAATGATTGGATTAAATCATCCAATG 720
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Unpublished (2002)
2 (bases 1 to 1200)
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
                                                                                                            ..
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 18-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids 1; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW930742 533 bp mRNA linear EST 18-MAY-20C EST355585 tomato fruit mature green, TAMU Lycopersicon esculentum CDNA clone cLEF40N15 5', mRNA sequence.
                                                                                                                                                                                                                                                                                     386 ACAACAAAAAACCIATGTTAGTTGCAGCAGAIATTTATCGTCCAGCAGCGATAAATCAAT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       446 TACAAACAGTAGGGAAACAAATTGATATTCCTGTATACAGTGAAGGAGATCAAGTAAAGC 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACAACAAATTGTAACTAATGCATTAAAACATGCTAAAGAAGAAGAACATTTAGACTTTGTAA 565
                                                                                                                                                                 86 AGATAATGATGCGTGAAGTAAGATTAGCGTTATTTGAGGCTGACGTAAACTTTAAAGTGG 145
                                                                                                                                                                                                                                    TGGAACCAATGAGGGACATTAGACGAGCTCTTCTGGAAGCAGATGTTAGCCTTCCTGTTG 210
                                                                                                                                                                                                                                                                   146 TAAAAGAATTTATTAAAACAGTATCAGAACGCGCATTAGGTTCCGATGTAATGCAATCAT 205
                                                                                                                                                                                                                                                                                                                              TAACACCAGGGCAACAAGTTATTAAAATAGTTCAAGATGAATTAACGAAGTTGATGGGTG 265
                                                                                                                                                                                                                                                                                                                                                          271 TCAAACCAGATCAGCAATTGGTTAAATTGTAAGTGATGAACTCGTGAAGCTAATGGGAG 330
                                                                                                                                                                                                                                                                                                                                                                                           331 GAGAGGTTCTGAGTTAACTTTTGCAAAATCTGGCCCCACTGTTATCTTACTGGCCTGGTC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACAAGGTGCTGGTAAAACAACAACAACTGCAGGTAAATTAGCATTATTGATGCGTAAAAAT 385
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                                                                                                                                          26 GCCTGCAAGCGACGATGCAAAAATGCGTGGTAAGGGTAAACTTACTGAAGCTGATATAA 85
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Έ
                                                                              Length 677;
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                                                                                                          0; Mismatches 247; Indels
                                                                              DB 14;
TAG_TISSUE-flowers pre-fertilized
TAG_SEQ=GCTTGACGGG"
100 c 192 g 172 t
                                                                           Score 178.8; DB 1 Pred. No. 2.5e-28;
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Clemson University
                               192 g
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                                                                                                            Conservative
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                                                                                            Similarity
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AW930742
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/tissue_type="fruit perioarp" (dev_stage="mature green (3-5 days pre-ripening)" (lab_host="solid green (3-5 days pre-ripening)" (note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; cLEF - Fruit were tagged at the 1cm stage and harvested 3-5 days prior to ripening; Fruit were out in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 AAACCTGCAGAAATAGCCCGACAAGGATTACAAGAGGCCCAAAAAGAAGAATGTAGATGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GGTCTACAAGGTGTTGGGAAGACAACTGTTAGTGCAAAGTTAGCTTTAT---ATCTAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.0%; Score 177.4; DB 10; Length 533; Best Local Similarity 59.6%; Pred. No. 5e-28; Matches 317; Conservative 0; Mismatches 212; Indels 3;
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                         /clone="clEF40N15"
/clone_lib="tomato fruit mature green, TAMU"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 others
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                                                                                                                                      /organism="Lycopersicon/cultivar="TA496"
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56.4 10173

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-WODEL=frame+_pD2.model_-DEV=xlp
-DE-Geng_1_/USFTC_spool_/US09943108/runat_21022003_151630_1801/app_query.fasta_1.647
-DB-Gengmbl -OFMT-fastap -SGFFTX=rge -MINMARCH=0.1 -LOOPCL=0 -LOOPEXI=0
-DOTALIGN=200 -TRR__MODEL=0.1 -MATRIX=blosum62 -FRANS=human40.cdi -LIST=45
-DOCALIGN=200 -TRR__SCORE=pct -THR__MAX=100 -THR__MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWI=pto -NDRM-ext -HEAPSIZE=500 -MINEN=0 -MAXIRN=200000000
-USREW-CS09943108 GCGN 1_1_3745_Grunat_2102003_151650_1801 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEC_SCORES=0 -WAIT -LOORIGG -DEV_INEOUT=120
-WARN_TIMBOUT=30 -THRRADS=1 -XGARDEXT=7
-YGARDOP=10 -YGARDEXT=7
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               GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                  using frame_plus_p2n model
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                                                                                                                                          Signal recognition particle polypeptide and polynucleotide Patent: JP 199923183-A 1 31-AUG-1999; SMITHKLINE BEECHAM CORP OS Unidentified
PN JP 1999235183-A/1
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                        Signal recognition particle polypeptide and polynucleotide.
E36050
E36050.1 GI:13022452
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Michael, T.B.
                                                               JP 1999235183-A/1. unidentified. unidentified
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PC A61K31/00
PC A61K31/00
PC A61K39/30
PC CI2N1/19
PC CI2N1/21
GOLN3/566//
PC CI2N1/21
PC CI2N15/00
PC CI2N15/00
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                                                                                                       unclassified
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ORIGIN
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ORGANISM
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No
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TITLE
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hypothetical protein, similar to RNA-binding Sun protein"
                    hypothetical protein, similar to polypeptide deformylase"
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5644. .6387
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                                             BCT 02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 303750)
Aoki,K., Oguchi,A., Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K.
and Kikuchi,H.
                                                                                                                                                                                                                 Staphylococcus aureus subsp. aureus N315 (sub_species:aureus N315,
Staphylococcus aureus subsp. aureus N315 genomic DNA, complete genome, section 5/10.
APRO13131 BA000018
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    .303750
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
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Alignment Scores:
Pred. No.:
Score:
Score:
Score:
Percent Similarity:
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Best Local Similarity:
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Conservative:
Ouery Match:
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Mismatches:
0
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Gaps:
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US-09-943-108A-2 (1-455) x AP003133 (1-303750)
Qy
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QY			360
qq	27326		27385
QY	361		380
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Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology; 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-857, Japan
(E-mail:Cohta@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454,
Pax:81-298-53-3454)
On May 29, 2001 this sequence version replaced gi:13875305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGKSILEKSIIKLLPEKISKLSSGEVIFDGKRIDTARKOLLDIRGNDIANIFGERA
TALNPVFTIKNOLVESIKSHKKISKREANNLAKDLLKKVGIARODEILNSYPHOLSGG
MRORVMIAMAISCSPKLLIADEPTTALDVTIQAQILDLLKELQKETQMAIMMITHDLS
                                                                                                                                                                                                                                                                                                                                                             BCT 07-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus subsp. aureus Mu50 (sub_species:aureus Mu50, strain:Mu50) DNA.
                                                                                                                               27566 AACGATATGAAGAAAATGATGAAACAATTCACTGGTGGGGGTAAAAGGTAAAAAGGTAAA 27625
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                                                                                                    AsnAspMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysGlyLys 440
ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
                                                                                                                                                                                                                                                                                                                                                        347235 bp DNA linear BCT 07-FEB subsp. aureus Mu50 genomic DNA, complete
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                                                                                                                                                                                                                                 Db 27626 GGCAATCAAATGCAAARTGTTAAAAGGTATGAATTTACGGTTT 27670
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Bacteria, Firmicutes; Bacillales; Staphylococcus.
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21311952
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AP003361 BA000017
AP003361.2 GI:14246761
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Ohta,T.
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                                                                                                                                      1 MetalaPheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLySMetArgGlyLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLys
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                                                                                                                                                                                                                     GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe
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                000
                  Mismatches:
                                     Indels:
                                                                                                US-09-943-108A-2 (1-455) x AP003361 (1-347235)
              100.00%
                Best Local Similarity:
                                     Query Match:
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HTFNLEKKQIMRFQQIQYLGGHKY VARKNAK I IELDNBAFDVIANYKLSKFAINOY
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6783. .776°
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100.00%
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IIHSRSFKDGFVSIQDKSSMFVAHIMNVDRHDHVLDACSAPGGKACHIAEVLMPEGQV
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PEIKYTQSKQHIESLVELQLEILENVKNNVKIGGEIIYSTCTIEQLENENVIYTFLKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein, similar to polypeptide deformylase"/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein, similar to RNA-binding Sun protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="ORFID:MW1098
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1919. 2207
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2400, 3335
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/gene="MW1099"
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EEEKDPDLEKYEE1EKKWKGIKDAPSLDKLDPLMTEKSFTNSKGIQGWKDYKELMGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELADY RFTKDSKGSSIKDVDAFFKGKKGIKRKVI ETHDDVKQVDYWYDPDGKKIGNS
NTPVFYAEIMTKYKDGKLVYASVEPGSYVIHKDDAIKYDDYSKLKKLSQLTKLDHPKP
             D 257810 AAAGGGCTAGATAAAGCTTAATATGAGTGAAAAGCAAATGATCATATTAAAGCGATTATC 257869
                                                                                                                                                                                                                                                                   DD 257870 CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACAACAATTGAATGTATCACGTAAAAAG 257929
                                                                                                                                                                                                                                                                                                                                                                  Db 257930 CGTATTGCTAAAGGGTCTGGTCGTTCATTACAAGAAGTCAATCGTTTGAAGAAACAATTT 257989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 257990 AACGATATGAAGAAAATGATGAACAATTCACTGGTGGCGGTAAAAGGTAAAAAGGTAAA 258049
                                                                                                                                                                                                                                                                                                                                      401 ArgilealaLysclySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
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                                                                                                                       LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIle 380
                                                                                                                                                                                                                               381 GlnSerWetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400
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Acki, K., Oguchi, A., Nagai, Y., Asano, K., Iwama, N., Baba, T.,
Kuroda, M., Hiramatsu, K. and Kikuchi, H.

Direct Submission

Direct Submission

Direct Submission

Direct Submission

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Direct Submission

Diamonday and Evaluation, Biotechnology Center; 2chome 49-10

Nishihara, Shibuya-ku, Tokyo 151-0066, Japan

(E-mail:oguchifalte-go.jp, URL:http://www.bio.nite.go.jp/,

Tel:81-33481-8423, Fax:81-3-34481-8424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus subsp. aureus MW2 DNA, complete genome, sprain:MW2, section 5/10.
APO44826 BA000033
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/organism="Staphylococcus aureus subsp. aureus MW2"
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Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Cui,L.,
Yamamoto,K. and Hiramatsu,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus subsp. aureus MW2 (strain:MW2) DNA. Staphylococcus aureus subsp. aureus MW2
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Lancet 359 (9320), 1819-1827 (2002)
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NEDVYELDKMKTIAVPLKKEDLAKHISEHKSNOPKRETTQVPIVNGPAHHQQFQKPEG
TYYEPREKKSTRKYTLSLIFSLIFSLIFSTANDANGFRANDANGFRAY
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RNIITKVMGTDKRVSPDLFIKRLNFYDYLLLNSDGLFDYVKDNBIKRLLVKBGTIEDH
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/codon_start=1
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                                        GATGGTTTAGAGCTATTCCATCCTGAACGTATGGCATCACGTATTTAGGTATGGGTGAT
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Listeria monocytogenes ATCC 19115
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Listeria innocua, genome and applications
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IGIAIKNFSNEPVSIEAGERVAQGVFQKYLVADTDIVANESRVGGVGSTGR"
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VGLHIFVDIFNAYGTQAVRPFKETWVARGFINTFDWFIFGSHVVALAAWLLGSPVLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVTLYVILALYYVARFVTQRMIKHAVQNLIPDSEEIIIASTIHFFQWRVAVTYKDHYY
VGRAFKRNISIYEKFDRLPVPDNEIIRSAKKDKNLAAFISFSKVYWWRIEBKLDGTYV
                                                                                                                                                                                      /translation="mrkmkrlymdetkitaf@ealvSwyeankrvlewrentepyriw
vssimlootkvDTv1pyfenrfmtQfpTmBSFvnaDeadilkAweGlGyySrvRvNLQTa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MDTGTHVVMGIALGALATVDPVVAGSSQAAIGIMTATIIGSQIP
                                                                                                                                                                                                                                           MKQVMADFSGEVPTDLTTILSLKGVGPYTAGAILSIAYNQAEPAVDGNVMRVIARVLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFTDLRYRSNGHYPFVAVVKLDDDLKIVSSYTGWIFSTEKLIKKLAPVSI"
complement(join(3130. .3147,3156. .3617,3625. .3630))
/gene="ino1691"
3130. .3147
                           /note="similar to A/G-specific adenine glycosylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to deoxyuridine triphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRGPEYAADYVRQQIERHGSFLHQVERKDPNK"
complement(join(3864. .4673,4680. .4685))
/gene="lmol693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to hypothetical proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(2129. .3123,3130. .3147)
/gene="lmol690"
2129. .2134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAC99768.1"
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/db_xref="SPTREMBL:Q8Y6J4"
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/db_xref="SPTREMBL:0816J3"
                                                                                                                                                                /db_xref="SPTREMBL:08Y6J5"
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                                                                                                           /protein_id="CAC99767.1"
/db_xref="GI:16411143"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3130. .3147
/gene="lmo1690"
complement(3130. .3147)
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/gene="lmo1691"
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/gene="lmo1692"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1948. .1953)
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                                                                                                                                                                                                                                                                                                                                                                             complement(850. .855)
/gene="lmo1688"
                                                                                                                                                                                                                                                                                                                                                                                                                            complement(850. .855)
/gene="lmo1688"
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/transl_table=11
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/transl_table=11
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%9ene="lmo1690"
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/gene="lmo1690"
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Baquero, F., Berche, P., Bloecker, H., Brandt, P., Chakraborty, T.,
Charbit, A., Checounal, F., Couve, E., de Darwar, A., Dehoux, P.,
Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L.,
Dussurget, O., Entian, K.D., Fsihi, H., Portillo, F. G., Garrido, P.,
Gattier, L., Goebel, W., Gomez-Lopez, N., Hain, T., Hauf, J.,
Jackson, D., Jones, L.M., Raerst, U., Kreft, J., Khuh, M., Kunst, F.,
Nedjari, H., Nordsiek, G., Novella, S., de Pablos, B., Perez-Diaz, J. C.,
Purcell, R., Remmel, B., Rose, M., Schlueter, T., Simoes, N.,
Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and Cossart, P.
Comparative genomics of Listeria species
L. Science 294 (5543), 849-852 (2001)
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HWDWTMNINAKALLFAGQEAAKLMQRHOSGKIISLSSIGSIRYLENYTTVGVSKRAAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCT 06-JUN-2002
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Direct Submission
Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALS91981 347050 bp DNA linear BCT 06-JUN-20
Listeria monocytogenes strain EGD, complete genome, segment 9/12.
ALS91981 ALS91824
GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400
                                 401 ArglleAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
                                                                                                                                    421 ASBASPMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysGlyLysGlyLys 440
                                                                                                                                                                                                                                              # 406 GGTGAAATGAAAAAAAATGAAGCAAATGACTGGTGGCGGCAAAAGGCAAAAAAGGCAAAA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87
Location/Qualifiers
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complement(join(845..1942,1948..1953))
                                                                                                                                                                                                                                                                                                                      441 ArgAsnGlnMetGlnAsnMetLeuLysGlyMetAsnLeuProPhe 455
                                                                                                                                                                                                                                                                                                                                                          346 ------AATCCATTCGCAATTTCAAAATGCCATTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Listeria monocytogenes"
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/db_xref="SPTREMBL:Q8Y6J6"
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complement(95. .841)
/gene="lmo1688"
complement(95. .841)
/gene="lmo1688"
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complement(845. .1942)
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/transl_table=11
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Listeria monocytogenes
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ACCESSION
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JOURNAL
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122056 GGGAAAGTAAACGAAGCTGACGTAAAAGAAATGATGCGGTGAAGTTCGCCCTTGCTCTACTA 121997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAGAAATTACAGGTGTCGTATTAACGAAACTAGATGGTGATACACGTGGTGGTGCCGCG 121337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220
                                                                                                                                                                                                                                                                                                                                                                                                             121996 GAAGCCGATGTTAAACTTTAAACGTTAAACAATTATTAAAACAGTAAGCGAACGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 LeuaspValThrGlyValThrLeuThrLysLeuaspGlyAspThrArgGlyGlyAlaAla
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                                                                                                                                                                                                                  1 MetAlaPheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLys
                                                                                                                                                                                                                                                                                                      GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe
               347050
331
64
55
                                                              Conservative:
Mismatches:
                                          Matches:
                                                                                                         Indels:
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    2.22e-93
1717.50
86.81%
72.75%
75.53%
                                                              Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYARFGLVLGTNGGSFPVFEKLFQTYTGGRFGNGRQWYSWIHVDDVVAAILFIFDHEQ
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321 GluLysLysMetargGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340   1:::      ::::::::	QY         401 ArgilealaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysClnPhe 420	AL596170,c LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS AL596170 AL596170 AL596170 AL592022 AL596170 AL59617	Dussurger.O., Entian, K.D., Fallin, H., Portillo, F.G., Garrido, P., Garrier, C., Entian, K.D., Fallin, H., Portillo, F.G., Garrido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T., Hauf, J., Jackson, D., Jones, L.M., Kaerst, U., Kurff, J., Kuhn, M., Kurst, F., Kurapkat, G., Madueno, E., Maitournam, A., Vicente, J.M., Nag. E., Purcell, R., Remmell, B., Rose, M., Schlueter, T., Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and Cossart, P. JOURNAL Science 294 (5543), 849-852 (2001)  PUBMED 11679669  REFERENCE C. (Dascripe of Listeria species Comparative promises of Listeria species Comparative Grant, P. J. (2001)  REFERENCE C. (2001)  AUTHORS Glaser, P., Prandenl, I., and Rusnick, C.	Direct Submission Submitted (00-704-2001) Microorganismes Pathoge Cedex 15, FRANCE E-mail: pglaser@pasteut Phone: +33 (01 45 68 8 Location/Qualian_Lis 1 .313450 /organism="Lis /db_xref="taxpl/db_xref"/db_xref="taxpl/db_xref="taxpl/db_xref"/db_xref="taxpl/db_xref"/db_xref="taxpl/db_xref"/db_xref="taxpl/db_xref="taxpl/db_xref"/db_xref="taxpl/db_xre

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100
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Indels:
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72.31%
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AGGFLEANVBLAABRGSLYIVEDVITTAFRFMYGGAQNYLGVTDDLTAMKKIIGGGLPI
GAVGGRVDIMEKYABLGBAYQAGTHAGNPASILSGTACLEVLQEGLYDDFREKXGSML
KEGIEKAAIKHGIAVTVNQIVGALTVYFTDEPVTNYAEAGATNGDLFGRFFKGMLEEG
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AYFYDVDGNKYIDYLAAFGPIITGHAHPHITBAITKAAQNGVLYGTPTKHBITPAKML
KEAIPSLEKVRFTNSGTBAWTIIRVARAYTGRDKIIKFAGCYHGHFDLVLVEAGSGP
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AVFINIGRGSAVELETLERASKEBQIAHFYLDVLPEBPLPAESYLWQASNVTITPHVS
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SFMLSHVKKAAFFYKMQKEEKWASEEPITELAGKTLVVAGTGAIGAKVAEFAQAFDME
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/translation="MKVLFTLDVPERLKNLQAEKPPDDTFYFESIDHFTNLGEVDVII
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/protein_id="CAC97024.1"
/db_xref="G1:16414296"
                           = 86.
                           /note="tRNAscan-SE vs 1.3 result - Cove score
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)Oin(11879. .12981,12990. .13016)
/gene="lin1794"
11879. .11884
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/gene="lin7792"
10476...1787
/gene="gsab"
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/db_xref="GI:16414295"
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complement.
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/gene="rRNA-23s"
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/gene="rRNA-23s"
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/gene="rRNA-16s"
complement(8850, .9335)
/gene="lin1791"
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/gene="lin1791"
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Db 138781 TIAGAAATTACCGGCGTTGTATTAACAAAATTAGACGGTGATACACGTGGTGGGCGGCAGCA 138722
                                                                                   DD 138661 GAAGCAATCGAAACGTTCCATCCCGATCGTATGGCTTCAAGAATTCTCGGCATGGGTGAT 138602
                                              138721 CTTTCCATCCGTTCAGTCACGAAAACCAATCAAATTCGTTGCTACCGGTGAAAAATG 138662
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                       LeuSerlleArgSerValThrGlnLysProlleLysPheValGlyMetSerGluLysLeu
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/db_xref="taxon:1642"
/note="seq 2058. original length: 3.011.208 replaced
by-seq 2058. o.000.001 to 0.349.980-seq 4032: 0.300.001 to
0.649.980-seq 4033: 0.600.001 to 0.949.980-seq 4034:
0.900.001 to 1.249.980-seq 4035: 1.200.001 to
1.549.980-seq 4036: 1.500.001 to 1.849.980-seq 4037:
1.800.001 to 2.149.980-seq 4038: 2.100.001 to
2.449.980-seq 4039: 2.400.001 to 2.749.980-seq 4040:
2.700.001 to 3.049.980-seq 4041: 3.000.001 to 3.011.208"
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Listeria innocua, genome and applications
Patent: WO 0228691-A 4037 11-APR-2002;
Pasteur Institut (FR)
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319
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                            1.69e-91
1647.00
84.62%
70.11%
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                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                            887
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ORIGIN
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80
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[ (bases 1 to 2739)

Honda, K., Nakamura, K., Wishiguchi, M. and Yamane, K.

Clonding and characterization of a Bacillus subtilis gene encoding a homolog of the 54-kilodalton subunit of mammalian signal recognition particle and Escherichia coli Ffh
93228695.
                                                                                                                  D14356
Bacillus subtilis orfl, ffh, rpsP genes for ORPI, Ffh and 30S-ribosomal protein S16, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAA2221.1"
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YEVSRQAVYDNIKRTEAMLEQYEEKLLLLKKFQERKEMFNKLKEIAASGSKEEBEITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFKVVKDFVKKVSERAVGODVMKSLTPGOOVIKVVOEELTELMGGEESKLAVAKRPPT
VIMMVGLOGAGKTTTSGKLANLLRKKHNRKPMLVAADLIYRPAAIKOLETLGKQLDMPV
FSLGDQVSPVELAKQALEKAKEEHYDFVILDTAGRLHIDHELMDELTINVKEIANPEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLVVDSWTGQDAVNVAKSFNEQLGLTGVVLTKLDGDTRGGAALSIRAVTNTFIKFAĞL
GBKLDALEPEPHPERAASKILGMGDVLTLIBKAĞSYDEDBRAKELBOKMEWASFTLDDF
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IINASRRKRIAKGSGTSVQEVNRLLKQPDEMKRAMKQMYNGKKKRFKLEFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAFEGLADRLQQTISKIRGKGKVSEQDVKEMMREVRLALLEADV
                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (03-FEB-1993) Kunio Yamane, Inst. Biological Sciences,
Tsukuba University; Tsukuba, Ibaraki 305, Japan (Tel:0298-53-6419,
Db 128241 GCTGAAATGAAAAATGATGAAGCAAATGACTGGTGGAGGAAAAGGTAAGAAAGGTAAA 128182
                                                     441 ArgasnGlnMetGlnAsnMetLeuLysGlyMetAsnLeuProPhe 455
                                                                                                                                                                                              rpsP; orfl; 30S ribosomal protein S16; ffh.
Bacillus subtilis (strain:168) DNA.
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bacillus subtilis"
/strain="168"
/db_xref="taxon:1423"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=experimental
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711. .2051
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/transl_table=11
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365. .697
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2157. .2429
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2157. .2429
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-10_signal
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Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Sekowska, A., Serori, S.J., Shin, B.S., Soldo, B., Scoroli, E., Takagi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Tosato, V., Uchiyama, S., Vandenbol, M., Vannier, P., Vassarotti, A., Vannutt, R., Wedler, H., Weitzenegger, T., Winters, P., Wipat, A., Yannuco, H., Yannae, K., Yasumoto, K., Yata, K., Voshikawa, H. P., Zumstein, E., Yoshikawa, H. P., Zumstein, E., Yoshikawa, H. and
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TGTVVASIDTGVEMNHPALKEKYRGYNPENPNEPENEMNYDAVAGEASPYDDLAHGT
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HPEWAPDVVNNSWGGGSGLDEWYRDWYNAWRAADIFPEFSAGNTDLFIPGGPGSIANP
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GNYAMSHNNILVMPPIKAPBGSELELÇPKSWHHLEDDPDZYSTVFULADERENWEQAGY
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NKLGVEKPSGKQKKKPVNPKKAKPSANTAVKHONKAIQPQVLPLKAQVSVVETGKSTY
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VELKGDVTKETALKPFVGYPGEIAYDDGTAENANSYFAAGNGWAVKMTLADGKDKGML
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FHAGIILNKGENELTATASTDNGTTDASSPITVTLDQEKPELTLDNPKDGGKTNKETL
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IDVNFDKPVISGLIPGEDKNLKAGESYKIAFSSAEDLDATFTIRMPLTNARASVQNAT
ELPLREISPGRYEGYWTATSSIKAKGAKVEVIVRDDYGNETRKTANGKLNMNTEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de I'Expression Genetique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANDE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKRSAVVSSLKVTADESQQDVLKYLNTQKDKGNADQIHSYYVVNGIAVHASKEVMEKV
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                                                                                                                                                                                                                                                                                                                    The complete genome sequence of the gram-positive bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kunst,F., Ogasawara,N., Yoshikawa,H. and Danchin,A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .208780
/organism="Bacillus subtilis"
/strain="168"
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/db_xref="G1:2633903"
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258. .4588
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/gene="bpr"
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Bacteria Firmicutes; Bacillales; Bacillaceae; Bacillus.

1 (bases 1 to 208780)

8 Kunst.F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolottin, A., Borchett, S., Bornise, R., Bernes, P., Bolottin, A., Borchett, S., Bornise, I., S., Euschi, C.V., Caldwell, B., Capuano, W., Choi, S.K., Codani, J.J., Concerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Enrlich, S.D., Emmerson, P.T., Entlan, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Frijta, M., Fupiet, C., Ferrari, E., Foulger, D., Frijta, M., Fupiet, C., Ferrari, E., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Handt, A., Hilbert, H.H., Holsappel, S., Haden, A., Golightly, E.J., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Liu, H., Masuda, S., Mauel, C., Medina, N., Mellado, R.P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawark, Ogawark, Ogawark, Odgaya, B., Park, S.H., Parroy, V., Pohl, T.M., Portetelle, D., Porwollik, S., Prescott, A.M., Prescan, E., Puinc, P., Purnelle, B., Rapoport, G., Rey, M., Sadaie, Y., Sato, T., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadaie, Y., Sato, T.,
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                                                                               1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1851 AAATCAATGACTGTTCTTGAAAAGAACAGCCGGATATTATCAATGCCAGCCGGCGGAAG 1910
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          261 LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu 280
                                                                                                                                                                                                                                                                                        301 ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
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                                                  281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
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Bacillus subtilis
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WIAGYLNELGFSIDKWDVYPGDPNVVGRLKGTDSADYYSLIINGHVDVAEVKEDEEWK
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GTFGASALEKNAKIIAGLGELRHWSINKSYFEFKPOTWINPAVIEGGRHAAFTADE
CRLWITUHFYPNETHDOVAAEIDEVYNRLSDSDIWLRENRPVFKWGGSSMIEDRGEIF
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                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="cab13410.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73213 GGGAAAGTCAGCGAACAAGATGTAAAAGAGATGATGCGTGAGGTCCGTCTTGCGCTGTT 73272
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                                                                                                                                                                                                                                                                                                                                                    /note="similar to hypothetical proteins"
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                                             /db_xref="SPTREMBL:031724"
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                                                                                                                                                                                                                                        9894. .10139
/gene="ylmC"
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IGAHSLLOSNSIVQNGYNITNQTGFGDPISNLFIVGGFPALWFSKRRIEDIETKNIQ
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NPEKKIKLATYASRCIENEILMYLRRNNKIRSEVSFYEPLNIDWDGNELLLSDVLGTD
DDIITKDIEANVDKKLLKKALEQLNEREKQIMELRFGLVGEEFKTQKDVADMMGISQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKKLKLRLTHLWYKLLMKLGLKSDEVYYIGGSEALPPPLSKDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to ABC transporter (ATP-binding protein)"
                                                                                                                                                                                                                                                                                                                                                                                                               /product="RNA polymerase sporulation-specific sigma-29 factor (sigma-E)"
                                                                                                                                                                                                                                                                                                                             cell-specific gene expression"
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/note="alternate gene name: spoiliG"
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                                                                                                                                                                                                                                                                                                                           /function="early mother cell-specifichote="alternate gene name: spoilGB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB13406.1"
/db_xref="G1:2633905"
/db_xref="SWISS-PROT:P06222"
                                                                                    /db_xref="SWISS-PROT:P13801"
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/db_xref="G1:2633907"
/db_xref="SPTREMBL:031723"
                                         /protein_id="CAB13405.1"
/db_xref="G1:2633904"
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/db_xref="G1:2633906"
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6605. .7387
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8531. 00
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/gene="ylmB"
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/gene="ylmA"
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9 (sites)
Nakasono,K., Masui,N., Takaki,Y., Sasaki,R., Maeno,G., Sakiyama,T.,
Hirama,C., Fuji,F. and Takami,H.
Gharacterization and comparative study of the rrn operons of
alkaliphilic Bacillus halodurans C-125
Extremophiles 4 (4), 209-214 (2000)
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Takami,H. and Takaki,Y.
Direct Submission
Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group; 2-15 Natsushima, Yokosuka, Kanagawa 237-0061, Japan (B-mall:takamih@jamstec-190.jp/jamstec-e/Dio/DEBPSTAR/FResearch.html, Tel:81-466-67-3899, Fax:81-468-66-6364)
On Jan 31, 2001 this sequence version replaced gi:10174886.
                                                       Takami, H., Nakasone, K., Ogasawara, N., Hirama, C., Nakamura, Y., Makui, N., Fuji, F., Takaki, Y., Inoue, A. and Horikoshi, K. Sequencing of three lambda clones from the genome of alkaliphilic Bacillus sp. strain C-125
Extremophiles 3 (1), 29-34 (1999)
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Reidentification of facultatively alkaliphilic Bacillus sp. C-125
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Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and
Horikoshi,K.
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Takami, H., Masui, N., Nakasone, K. and Horikoshi, K.
Replication origin region of the chromosome of alkaliphilic
Bacillus halodurans C-125
Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)
99356711
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Takami, H., Takaki, Y., Nakasone, K., Hirama, C., Inoue, A. and
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                   to Bacillus halodurans
Biosci. Biotechnol. Biochem. 63, 943-945 (1999)
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Extremophiles 4 (2), 99-108 (2000)
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Takami, H.
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Takami,H., Nakasone,K., Hirama,C., Takaki,Y., Masui,N., Fuji,F.,
Nakamura,Y. and Inoue,A.
An improved physical and genetic map of the genome of alkaliphilic
Bacillus sp. C-125
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                                                                                                                                                                                                            74113 GAACAAAAATGAGAACGATGAGCTTCACATTGGACGATTTTCTGGAGCAGCTCGGGCAA 74172
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                                             73813 GTTGTCGATTCAAFGACCGGTCAGGACGCTGTGAATGTTGCCAAAAGCTTTAATGAACAG 73872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AsnAspMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysLysGlyLys 440
                                                                                                                                                                                                                                                                    261 LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet 360
                     201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220
                                                                                                     ValvalaspSermetThrGlyGlnaspalaValasnValalaGluSerPheAspAspGln
                                                                                                                                                                                    241 LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla
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Bacillus halodurans
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Bacillus halodurans genomic DNA, section 9/14.
AP001515 BA000004
AP001515.2 GI:12641879
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Extremophiles 3 (1), 21-28 (1999)
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Takami, H. and Horikoshi, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210374 GGGAAAGTAAGTGAACATAAAAGAAATGATGATGCTGCTGCTCTGCTCTCCTA 210315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210254 CTCGGTCAAGAAGTCATGAAAAGCTTGACACCTGGACAACAGGTCATCAAAGGTCGAAT 210195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210194 GARGAGGGGCGGTGATGGGAGGCGAGCAAAGCAAGCATTGCGAGGCAAGCCG 210135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210314 GAAGCGGATGTAAACTTTAAAGTGGTGAAGCAATTCATCGCCAATGTGAAGGAAAAAGCC 210255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLys 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 GluAlaAspValAsnPheLysValValLysGluPheIleLysThrValSerGluArgAla 60
                                                                                                                                                                                                                       /product="heat shock protein class I (low molecular weight)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe
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Matches:
Conservative:
Mismatches:
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Gaps:
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STTFS"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                   209654 CICICGGITAAGGCGGITACGAACACGCCGATCAAATTIGCCGGGATGGGTGAAAAGATT 209595
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                                                                                                                                                          209894 AAAGAAGAGCATCACGACTATGTGTCCATACAGCTGGACGTCTTCACATCGATGAA 209835
                                                                                                                                                                                                                             209834 GAGCTGATGGATGAACTGCAACAAGTAAAGGAAGTGGCCAAGCCAGGTGAAATCTTGCTC 209775
                                                                                                                                                                                                                                                                                      209715
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210074 CITGCCAACCATTTGCGGAAAAAGCACAATCGGAACCCGATTCICGTCGCTGCCGATATT 210015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet 360
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                                                                                                                                         LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200
                                                                                                                                                                                                 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220
                                                                                   TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180
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                                                    210014 TATCGTCCGCCTGCGATTAAACAGCTTGAGACATTAGGTAAACAATTAAACATGCCTGTG
                                                                                                                                                                                                                                                                                                                 LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla
                            TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal
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                                                                   Bacillales; Bacillaceae; Bacillus
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FDMIKECESNIVDIYLMPKDISKLISKKTFFYSMKDKLNNLRINVIONPEVEKDTLK
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QIMLGLPGDNAEKDI ETTRKVI CMKPNICRIYPALVIKDTAMEKMYNRGIYKPYDIEB
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DEPDAKYSSNKTKYYESKSEHQKILSEIELLKEKTSNSDVAKNKLYKEIEDLDNSIVN
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KLINYLKSKNLGRATFLPLNIIKGRKLNISDATRHEKGFIGIASELIDYDSTFLPAVN
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REIEEELNIELINNVSQALEQSSNKIIENKKVVKELDNICLDLTDTIHGEKIELTKIKER
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/note="rncs"
                                                                                                                 444. .1136
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Nolling,J., Breton,G., Omelchenko,M.V., Markarova,K.S., Zeng,Q.,
Gibson,R., Lee,H.M., Dubois,J., Qiu,D., Hitti,J., Wolf,Y.I.,
Tatusov,R.L., Sabath,F., Doucette-Stamm,L., Soucaille,P.,
Daly,M.J., Bennett,G.N., Koonin,E.V. and Smith,D.R.
Genome sequence and comparative analysis of the solvent-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium acetobutylicum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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LeuaspvalThrGlyvalThrLeuThrLysLeuaspGlyaspThrArgGlyGlyalaala 260
                                                          CTCGGTGTGACAGGTGTCATCTTGACGAAGCTTGACGGCGATACTAGAGGCGGAGCGGCC 780
                                                                                                         LeuSerlleArgSerValThrGlnLysProlleLysPheValGlyMetSerGluLysLeu 280
                                                                                                                                    281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300
                                                                                                                                                                                                                                             ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
                                                                                                                                                                                                                                                                                                                                                       GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
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Childress, D., Zeng, Q. and Smith, D.R.
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/db_xref="ATCC:824"
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AE007684 AE001437
AE007684.1 GI:15024715
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/rranslation="Medefesigolinthgvrgelklyplfddinreddldsvyddei
KRVISVKKQPNKLILKLBGIDTLDEAVRYKNKYIKVLREDAVELKEGQYFIKDIIGCN
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/gene="CAC1757"
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VIMAVGLQGAGKITMCGKLSLSLKKKNKKPLLVACDIYRPAAIKQLEVVGKSIDVPVF
SMGDKVNPVDISKAAMKHAKENGLNVVIIDTAGRLHIDDQLMNELENIKSEVNPKEIL
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                                                                                                                                                                                                                                                      ILITSDIGVETSLYIIDKLKEKIKENKVKDPSLVNDCLKEVIKDILGDKKGSLMPKQI
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/protein_id="AAK79718.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Uncharacterized conserved protein, YLXM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Signal recognition particle GTPase Ffh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
    QFIVITHRKGTMEASDVLYGVTMEEKGVSKVISLDLDSDRENVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="Predicted nucleic acid binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVTFKVDADKVNAWMKNGAQPSETVKKLLDKSGVTTK"
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9718. .10218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Ribosomal protein S16"
                                                                                                                                                                                                                                                                                                                                      PVEFVGVGEGIDDLQEFNPSDFVEALF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s.subtilis ortholog"
/protein_id="AAK79719.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAK79721.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CAC1753"
/codon_start=1
/transl_table=11
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/gene="CAC1755"
/note="rpsP"
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/transl_table=11
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/gene="CAC1755"
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/gene="CAC1753"
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/gene="CAC1754"
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/gene="CAC1754"
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                       5352. .7263
/qene="CAC1752"
                                                                                                        /gene="CAC1752"
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                                                                                                                                /codon_start=1
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7710. .9059
                                                               /note="ftsY"
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/translation="MKMKTRDLTLIPIFAALTAIGAFIKIPIPIVPFTLQYFFCALGA
ILLGAKRGALAQIIYVLVGLLGIPVFTQGGGPSYVFQPTFGYLIGFIFGAYIIGKITE
NLKTINIKNLFLAGILGLLVIYLFGVSYMYVIYNFYLGDAMSLLSAVSIGAIACLPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="319 aa, similar to pir:E70384 biotin synthetase (EC 2.8.1.6) from Aquifex aeolicus (332 aa); 43.4% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MDFILKMKDKSLKNIKLTREEGLRLFNSNLEELIKEANNIRKEI
HGDGIDLCSIINGKSGRCGEDCARCAQSKYHKTNISEYPLLDYEKIKKVAKRNEDEGV
HRFSIVTSGRGLYGEEFERVITYYSNLNKELKINLCASHGIINKESLIKLKKAGVKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHULETSRNYYDKICKTHSYEERVKTIKNAKEAGLEVCSGGIIGLGETILDRIDLAIT
LRELEIKSTRINTLSAKGTKLOMIPLNEBEILRTAVFRINPEAKIRLAGGRYLL
KNEGENAPKAGANATIGULLITCGNKIKDDKRLIENIGMRIF"
COMPLEMERT (1754. . 2308)
                                                                                                                                       /note="228 aa, similar to sp:BIOD_METJA DETHIOBIOTIN
SYNTHETASE (EC 6.3.3.3) (DETHIOBIOTIN SYNTHASE) (DTB
SYNTHETASE) (DTBS) from Methanococcus jannaschii (248 aa);
33% identity in 221 aa overlap
CPE1543"
                                                                                                                                                                                                                                                                                                                                                                                                     IKEKNGLIPLDCEEVMKISGLKESYENMVSYILENPYSPHLASEVEEVSISMEKIKKD
YKSVRDKYDFILCEGSGGIVCPISFSEKKLMLEDIIKEFNLQIILVSNSGLGTINVTV
LTVSYLRNLGLKVKGIILNKFNKSDIIHRDNKKIIKELTGVNNISTVPKIEDIEKYDL
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                                                                                                                                                                                                                                                                                                        /product-"dethiobiotin synthetase"
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/db_xref="c1:18145206"
/translation="MBKGVYIIGTNTDIGKTFISGLILKKIREBGRNAGYYKAVLSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="184 aa, similar to sp:BIOX_BACSH BIOX PROTBIN from Bacillus sphaericus (215 aa); 43.4% identity in 173 aa overlap. Putative N-terminal signal sequence and 4 putative transmembrane regions were found by PSORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="CPE1546"
complement(2694. .3785)
/gene="CPE1546"
/note="CPE146"
/note="363 aa, similar to sp.:YPUA_BACSU HYPOTHETICAL 31.3
/note="1658 PROTEIN IN LYSA-PPIB INVERGENIC REGION (ORFX19) from Bacillus subtilis (290 aa); 31% identity in 271 aa overlap. Putative N-terminal signal sequence was found by
                           for gas gangrene'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved hypothetical protein"
/protein_id="BAB81252.1"
/db_xref="GI:18145209"
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/protein_id="BAB81251.1"
/db_xref="GI:18145208"
                        /note="anaerobic pathogen complement(87. .773)
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complement(2694. .3785)
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/db_xref="taxon:195102"
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                                                                                             complement(87. .773)
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CPE1544"
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                                                                                                                      /gene="bioD"
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                                                                       /gene="bioD
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13 DNA, complete genome, section 7/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (15-FBB-2001) Tohru Shimizu, Institute of Basic Medical
Sciences, University of Tukuba, Department of Microbiology; 1-1-1
Tennohdai, Tsukuba, Ibaraki 305-8575, Japan
(E-mail:tshimizu@md.tsukuba.ac.jp, Tel:81-298-53-3354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                              8547 AATGATATTGAGATCTTTCATCCTGATAGAATGGCATCAAGAATACTTGGTATGGGTGAT 8606
                                                                                                                                                                                                                                   8727 AIGAAAAAGITAGGACCTATAGGTAAGCTICTTGAAATGGTTCCAGGTTTTAATAGTAGT 8786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8904 TCGAGGAAAAGAAGAATAGCTCTTGGATCAGGTACTACGGTTCAAGAAGTAACAAATA 8963
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                   LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu 280
                                                                                                                 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300
                                                                                                                                                                                                       ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
                                                                                                                                                                                                                                                                                                     321 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 ---MetLysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAla 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 IleIleGlnSerMetThrProAlaGluArgAsnAsnProAsp-----ThrLeuAsnVal 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerArgLysLysArgIleAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeu 416
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                                                                                                                                                                                                                                                                                                                                                                                                   341 ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLys---
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Location/Qualifiers
1. .296750
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AP003191 BA000016
AP003191.2 GI:18146729
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Shimizu,T.
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VERSION
KEYWORDS
SOURCE
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FEATURES
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SQYGSGGVLKGIEDIFFNFYGGVSKATGGPCWSAGMRAQKYDFGDSVSNSLEDMINSK
NIFLWGKNPANTTIHTWAILNKAKKNGSRIIVIDPINFQSAKLGDIHVKIKPGTDGAL
AWAMAKIIISKGLQDKDFINKYVLGFQEYKDHLENFDLDYLSDECGIEIEDIEKLFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKLESIIGMKELKEFIDKIENNFKVQKIREKLGLKTTQISLNMIFAGNAGTGKTNAAR
ITFEYLYALGMIKENIFKEVSKADFIGEGISNTARRTNEIIESALGGVLFIDEAYSLC
TDENDKAGREIVDALLKGIEDNRDNITVILAGYEKDMETFLSFNQGLKSRFPNVIKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /hote="662 aa, similar to pir:866017 formate dehydrogenase homolog yyaE from Bacillus subtilis (667 aa); 32.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFKSGEVGENREFYVSNINEFIEEPKKYSLSVEDSNAPIKIMVIANSNLMNQLPNLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNNSIDKVEFKVCFDMFMTDTASKCDLFIPCTNTLESEDMVFSSMTNPYLIYNEKIIE
                                                                      VTNNYNILLFQCQQQQTIKFMSKINDLDYNYCAMKESLNQMNDKLQQILKDTGKQLEE
SGLLEKALNGIKNVLVDIKDFLVNMFSSASEKVKDCITYDENGNIVIKTGNNSDESKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMDASKKYLVNKERAIDLLEKDNFNFKVSAKFDLEEKLKEIIGLEEVKEFLRSQYKLI
VAQEKRKSVGVNTKIEGNLNMIFAGNPGTGKTSIARLVAEMLNSMGLLKVGQLVETDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIVILAGYEEEMENFFDVNIGLRSRFPLWTKFEDYNPNELLEMAIKLYEAKGFKLSKN
GYSELKKNFVEIYENADAOSGNGRMYRNYVEOLLRNOSIRLAESDISVYEMNLINTKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NMVFTGESGTGKKTVLNIYSEMLISMGIIKAKNIVQIDKYEFMAMINSGMKVEDILNK
HVGKILYIDKWNTFFGEERYNEIVSDLIKFIDNNSNRIVIVLGGIRGKMKDLIITNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MEVLSHGCTLDCFDCCKFNVYKEGSEILKIEGDKEHPFTKGLIC
KKGVAHLNRLNHKDRIYTPLLKNNGVWEEISFEDALEIMKEKLEYTKEKYSSKSILYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCEKNSSIYLGYGMQKYKNGGNTIRAIDALGALTGQIGYKGGGVNYANKVLSRILDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYDDVAWENKKFKTPSGKFELASKRALKECGSLTPTYLSPRIKENCFRLLTNHSKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSQHYIDVDEKAKVYLNENMIRKFSLICGEKVKLKSRTGEITAICSLDNGVQDYVALM
NNLTEVTGSMLANALLTSGVNNADVKADAPFKVTGTAALAGILKGFEDASGEELSLPK
                                         KEAAREEISLINNLSNAKTKDGQTLGKDEAAVVVNDIKTDVIKDKPKNDEEIGKIVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MLQKNIFVERKDMVNKEIIENGFFKIEKKLNEEFIGQKTFNKEL
CDYFKEKIEEDSKGIILIVEERDIFKNSVLKYFFEELNYKFVKNSKIDEIDLAAYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLGYNAFLTDLYEKLNNDSQCLVFKNTDKASEDILNVLSGISPNSCIMLKDNYVIKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLVBABBIDEDIVNKIICNNKFFIFLYNKDKGEELBIIDNEFLINKDKTLYRKALSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKNKVIKKKLLKEINKVKELFDIDIIIGVDENPDVEEKSGVCTYIEDNFREKGSLSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QYISYKICKPIINIIRKEAIEANSRLLIYVEDDEIFCKSNDEVYDLSKYSNPTLEEVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYNPSEMYEIAVNIAKSKGYRIAKSAKAGLIELFTKNQMVGKSDLGNARFVRNIVENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSFVSDIPGETSKKTEEKFKEALGGVLFIDEAYTLANDSIGREAIETLLKLIEDYSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKAMNAIKYDNHFDLEKKLNNLIGNEELKDFLRGQYKLMKIREKRKKLGFQVDLNKYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNYRFPIWVDFGNYNERELYDIASSTLVKKGFTLDEEAETALENAIGDIQKRMGELAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNGLMIKQFLDSLVRVQSIRVCDEDFDINTINRIISEDILKSTEIFLKKNTTQNGSF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PREKLMDEYYFFRELAKRMNLKGYPSLSKKDYLSKVIEPLMSYNKDITLDYLKNNPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                             in
                                                                                                                                                                                                                                                                                                                                              /note="1145 aa, similar to gp:AB015670_7 Bacillus sp. genes for Chase, CGTase, MBP and 15 ORFs, partial and complete cds from Bacillus sp (549 aa); 45% identity i 522 aa overlap.Also similar to pri:2516401x stage V sporulation protein K from Bacillus cereus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="364 aa, similar to pir:A71345 probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/product="probable formate dehydrogenase"
/protein_id="BAB8125.1"
/db_xref="GI:18145211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
/product_"stage V sporulation protein K"
/protein_id="BAB81253.1"
/db_xref="G1:1814210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVGWWKKHGNPNFLTESGISDMGGQITYNETFIEIENI"
                                                                                                                                                        EESIQDKPQTQSNDNNQNQENEQGQNQTK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identity in 667 as overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7634. .9622)
/gene="fdh"
                                                                                                                                                                                                  complement(4141. .7578)
                                                                                                                                                                                                                                                                            complement(4141. .7578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(7634. .9622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .11127
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                                                                                                                                                                                                                                       /gene="spoVK"
                                                                                                                                                                                                                                                                                                                     /gene="spovk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="prs"
10033. .111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="prs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="fdh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPE1547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPE1548
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/protein_id="Bab81255.1"
/db_xref="G1:18145312"
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RFSNOEGKYNIPOGYNGRDIYILCDIGNYSCTYKNEGFENHKGPDEHEQDIKRTVSAI
                                                                                                                                                                          RGKARRITVIMPLLYESRQHRRKGRESLDCALALQELERLGVDEVLTFDVHDPNVQNA
IPLMSFENFYPTYDIVKSLIHNEKDLELDKEKLLVISPDTGAMDRAIYYSSVLGVDVG
                                                                                                                                                                                                                       LFYKRRDHSRIVNGKNPIVKHEYMGRDVDGKDVLIVDDMIASGESVLDIAKELKGRNA
RNYYVATTFSFFTEGLEKFNKFFNDGIIKSVYSTNLTYIPEELNAAPWFKAVDLSDFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DD 184629 TATAGACCTGCAGCTATAAAGCAATTACAGGTTGTAGGAAAACAAATAGAATATACCAGTA 184570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 184866 GTTGGTGAGGAAGTATTAAATAGTTTAACTCCAGGTCAACAGGTTATTAAAATAGTTAAT 184807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 184746 CCAACAGTGTTAGTTAGTTAGGTCTTCAAGGTGCAGGTAAAACAACAACTATGGCTGGAAAA 184687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 184806 GACGAATTAACAACTCTTATGGGAGAGACTGAGAGTAAATTAAAATACTCAGACAAIGGA 184747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184569 TTCTCAATGGGAGATAAGGTTAAGGCTGTAGATATTGCCAAAGCTGCAATAGAGCATGCA 184510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLys 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAspIle 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 TyrserGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 TyrargProalaalaalaaleasnGlnLeuGlnThrValGlyLysGlnIleaspIleProVal 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlualaaspValasnPheLysValValLysGluPheIleLysThrValSerGluargAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGln 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetalaPheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLySMetArgGlyLyS
                /transl_table=11
/product="probable phosphoribosyl pyrophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296750
279
72
86
8
                                                                                                                                                                                                                                                                                                                                                                                  /note="353 aa, no significant homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                     ARIINRLNYDKSVASYMDATNIIQRLLDEK" complement(11177, .12238)
                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
/product="hypothetical protein"
/protein_id="BAB81256.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
                                                                                                                                                                                                                                                                                                                                  complement(11177. .12238)
/gene="CPE1550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-943-108A-2 (1-455) x AP003191 (1-296750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                  /gene="CPE1550"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.39e-73
1382.00
78.88%
62.70%
60.77%
                                                                synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
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                                                                                                                                                                                                                                                                                               gene
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DD 184269 CTTTCAATAAGAGACATTACTGGTAAACCAATTAAATTTGTTGGTGTGTAGGGAAAAGATG 184210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184209 AGTGATATTGAAGTATTCCATCCAGATAGAATGGCTTCAAGAATATTAGGAATGGGAAT 184150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D 184149 GTCCTTTCTTTAATAGAAAAGCTCAGCAAGCTATTGACCAAGATGAAGAAGAGAAAAAGTTA 184090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 184089 AGTCAAAAAATGTTAAATCAAGAATTTAACTTTGATGACTACTTATCAGCTATGGATCAA 184030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 184509 AAAGACAATGGAAATAACGTTGTTATAATAGATACCGCTGGTAGACTTCATATAGATGAA 184450
                                                                                   DD 184449 GAITTAATGCAAGAGTTAAAAGATGTTAAAAGAAGTTTCAAATCCTAGTGAAATATTA 184390
                                                                                                                                                                                        D 184389 GTAGTTGATGCTATGACAGGTCAAGATGCTGTTAATGTAGCTGAGACATTTAATGTAATGCTG 184330
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| Db 183792 TTABARAGCCTATGRARTGATGARARAGARGGRAATGARAGGARATGARATCATTCCARARART 183733
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                                                     201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220
                                                                                                                                                            ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln 240
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Search completed: February 25, 2003, 02:59:00 Job time: 4087 secs

Run on:

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Command line parameters:
-MODEL=frame+_p2n.model_-DEV=xlp
-Q=Cogn2_1/T90/app_query.fasta_1.647
-Q=Cogn2_1/T90PC_gFOO_1/W109943108/runat_21022003_151629_1790/app_query.fasta_1.647
-D=N_Geneseq_101002 -QFNT=fastap -SUFFIX=rng -NINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=blts -SFNRT=1 -END=-1 -MATRIX=blosum62 -TRNS=bluman40.cdi
-LISS=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALXIEN=20000000
-USES=UCOG1.OFFNT=PCT -NORM=ext -HEADSIZE=500
-USES=UCOG343108_GCGN_1_1_396_dcunat_21022003_151629_1790 -NCPU=6 -ICPU=3
-NO_XLDXY -NO_MMAP -LARGEQUERY -NGG_SCORES=0 -WALT -LONGIGG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPQP=10 -XGAPEXT=0.5 -FGAPQP=6 -FGAPEXT=7
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2274
1 MAFEGLSERLQATMQKMRGK......GKKGKRNQMQNMLKGMNLPF 455
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                            using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Η,	ر د	ST S	Staphylococus aut	000	ocūa	us e	Enterococcus iaeca Enterococcus faeca	4 44	Bacillus lichenifo	2CFE 28 coding seq	Streptococcus pneu	CFR 28 anding seam	Streptococcus pneu	S. aureus ffh codi	Streptococcus pneu	DNA encoding Strep	Streptococcus poly	S. phenmoniae deri	Streptococcus pneu	C glutamicum codin	c glutamicum codin	E. coll growth and	Staphylococus anr	Pseudomonas aerugi	Haemophilus influe	Haemophilus influe	Salmonella typni u N meninditidis na	Nejsseris meningit	Neisseria meningit	Genomic fragment #	Propionibacterium	Buchnera sp. genom	Borrelia burgdorfe	Mycoplasma genital	Helicobacter pylor	chia sp. E/	Staphylococcus aur									probial	1115			
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                                                                                                                                                                                                                                                                                                                          New Staphylococcus aureus Signal Recognition Particle (SRP) with protein (ffh) and RNA (ffs) components - the SRP gene and protein useful as diagnostic reagents and for prevention and treatment of Staphylococci infections which cause otitis media, septic arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 28; 35pp; English.
   98EP-0306741.
                                                          97US-0927216.
                                                                                                                     (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxic shock syndrome
                                                                                                                                                                                                                                    1999-169238/15.
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                                                          10-SEP-1997;
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24-AUG-1998;
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Sequence 1368 BP; 521 A; 186 C; 288 G; 373 T; 0 other; 1368 455 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: 3.47e-197 2274.00 100.00% 100.00% 100.00% Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.:

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            LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu
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                                                                                                                                          TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla
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                                              LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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                                                                                               Staphylococcus aureus DNA for cellular proliferation protein #1643
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                                                                                                                      Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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                        AAS55331 standard; DNA; 1368 BP
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26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOY-2000; 2000US-253625P.
22-DEC-2000; 2000US-25363P.
16-FEB-2001; 2001US-269308P.
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                                                                       (first entry)
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Xu HH;
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Yamamoto RT,
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RESULT 2
          AAS55331
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US-09-943-108A-2 (1-455) x AAS55331 (1-1368)

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LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIle
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                                                         GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys
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26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-25363P.
16-FEB-2001; 2001US-269308P.
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Xu HH;
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programmes. The antisense nucleic acid sequence is also useful for homologous nucleic acids which are required for cell prolif a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                    Sequence 1365 BP; 518 A; 190 C; 285 G; 372 T; 0 other;
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Yamamoto RT,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, themselves and the encoded proteins. The prokaryotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella promunoniae, Pseudomonas aesuvignosa and Enterococcus faecalis. The prokaryotis used in prolification of potential new targets invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to clamitify proteins used in prolification, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part contraction in the contraction and the printed specification, but was obtained in electronic forms directly from MIPPO at the contraction and the contraction and the contraction and the contraction are contractined in electronic forms directly from MIPPO at
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AC ABQ70511;
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DT 29-AUG-2002 (first &
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DE Listeria monocytogene
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KW Antibacterial; Listeri
KW infection; ds.
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The present invention relates to nucleic acid sequences (ABO67188-ABO71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (portential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.

Note: The sequence data for this patent did not form part dit ne printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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treatment and prevention of infection, also related
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Matches:
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Mismatches:
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The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
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Listeria innocua contig DNA sequence #7
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bacterial infection;
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W.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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23 - MAY - 2000; 2000US - 206648P - 26 - MAY - 2000; 2000US - 207727P - 23 - OCT - 2000; 2000US - 242578P - 27 - NOV - 2000; 2000US - 253625P - 22 - DEC - 2000; 2000US - 253625P - 16 - FEB - 2001; 2001US - 269308P - 2001
                   21-MAR-2001; 2001WO-US09180.
                                                                                                                (ELIT-) ELITRA PHARM INC
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Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                         AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300
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                  255
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                                                                          LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu
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 LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGln
                  196 crassrrcrsarscrarscrarcrrrancesscrassasserrarranancera
                                      AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro
                                                        LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle
                                                                                                                                                     TyrargProalaalaIleasnGlnLeuGlnThrValGlyLysGlnIleaspIleProVal
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antibiotic;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential cannot be themselves and the encoded proteins. The prokaryotes used are schemically staphylococcus aureus, Salmonella typhi, Klebsiella promuoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The prokaryotic development. The antisense nucleic acids can also be used to antibiotic development. The antisense nucleic acids can also be used to chantify proteins used in proliferation, to express these proteins, and to obtain antibodise capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Wote: The sequence data for this patent did not form part
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New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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Matches:
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                                                                             Claim 27; Seg ID No 3890; 511pp; English.
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Best Local Similarity:
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella premomentae, Pseudomonas aeruginosa and Enterococcus facealls. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Sesential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic
    GATCAAARGCTAGGCGGCGTTAAAGGCAAGTTAGGTAAGATAG---GCCATGAATCGT 1377
                                                                                                                                                                                                               Enterococcus faecalis DNA for cellular proliferation protein #555
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20000S-207727P.
20000S-242578P.
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antibacterial;
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P-PSDB; AAU35268.
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Yamamoto RT,
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Pred. No.:
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AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100
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1021 GITATGGGCATGGGACCGATTGAAGACTTATTAAAAATGATCCCTGGAATGAGTAACATG
                                                                         LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIle
                                 ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet
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86
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A computer readable medium has been developed which has recorded on it. 982 nucleotide sequences isolated from the Enterococcus facetlis genome. AAXI2938 to AAXI3919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based 1321 GATCAAATGCTAGGTGGCGGCGTTAAAGGCAAGTTAGGTAAAATG---GCCATGAATCGT 1377 420 New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 401 ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 1201 AGAATTGCAGCTGGTTCAGGAAATAGTGTGGTTGAAGTCAATCGTATGATTAAACAATTT 421 AsnaspMetLysLysMetMetLysGlnPheThr-----------------Enterococcus faecalis, contig, detection, Enterococcal infection, vaccine; attenuation; computer readable medium; ds. Enterococcus faecalis genome contig SEQ ID NO:37

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system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the can be used to approperlides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal infection.
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                               261 LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu
                                                                                                   281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
                                                                                                                                                                     ValleuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu
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2001US-279526P.
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27-MAR-2001;
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Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                             Monitoring differential
                  WPI; 2002-416684/44.
                                               sequenced tag array
     Clausen
      Ä,
      Berka
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Claim 4; SEQ ID NO 1847; 200pp; English.

The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring of Johal expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in which Bacillus cells adapt to changes in culture conditions, in which Bacillus cells adapt to changes in culture conditions. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO environmental stress or other physiological provocation. Extensive follow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information available. This sequence represents a genomic sequence tag (GST) used the method of the invention.

ftp.wipo.int/pub/published\_pct\_sequences.

other; 0 E-i Sequence 1136 BP; 338 A; 263 C; 326 G; 209

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61 GGAAAGGTAACGGAGCAAGACGTCAAAGAGAGAGTGCGCGAAGTCCGTTTAGCGCTCCTT 120
                                                                                                                                                                                                                                                                                       GAAGAGCTGACGGAGCTGATGGGCGGCGAGGAAGCAAGATTGCCGCTGCAAAAGGTCCG 300
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                                         Conservative:
Mismatches:
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Matches:
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TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal
                                                             TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla
                                                                            LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conding polypeptides (AAMO1102-CAMO1114), which are essential for the viability of a bacterial cell wall. The acronym CFE stands for "CDG For Expression", where CEG stands for "Conserved Essential Gor "CDG For acids are useful for detecting the presence of proteins essential for the nucleic acids are useful for detecting the presence of proteins essential for the biological fluids, blood, serum, nose, ear or throat swabs with ligands, and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nucleotide sequence of interest is essential for viability of a bacterial cell or whether it resides within an operon, by integrating an exogeneous nucleotide sequence comprising a portion of an open reading frame of the genomic sequence of interest corrising 200-500 base pairs) into the genomic sequence of interest which confers a selectable phenotype to the cell, and determining cell corresponding and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids antibiotic resistant bacterial infections.
                                                                                                                                                                                                                                                                               bacterial
antibiotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to nucleic acids (AAH90701-AAH90918)
                                                                                                                            Bruccoleri
                                                                                                                                                                                                                                                                         Nucleic acids encoding conserved essential genes involved in replication which are potential targets for the treatment of resistant bacterial infections -
                                                                                                                            Davison DB,
                                                                                                                         BA,
                                                                                                                         Dougherty
                                                                                                                                                                                                                                                                                                                                                                                               Claim 30; Fig 49; 380pp; English.
                                                         (BRIM ) BRISTOL-MYERS SQUIBB CO.
99US-0174089.
                                                                                                                         Pucci MJ,
                                                                                                                                                                                                               WPI; 2001-496721/54.
                                                                                                                         Dougherty TJ,
   30-DEC-1999;
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Sequence 1605 BP; 484 A; 317 C; 393 G; 411 T; 0 other; Length:
Matches:
Conservative:
Mismatches: Indels: Alignment Scores: .. 0 

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Gaggaactgacagcogtittasgttctgatacggcagaaattatcaagtcacctaagat
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TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal
                                                                                                                                                                                                                                         CAAACTAATCATAACGACTATGTCTTGATTGATACTGCGGGTCGTTTGCAGATTGATGAG
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                                                                           TITGCACTIGGAACAGAAGTACCAGCIGTTGAGATTGTACGTCAAGGTTTGGAGCAAGCC
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GAGGAACTGACAGCCGTTTTAGGTTCTGATACGGCAGAAATTATCAAGTCACCTAAGATT
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Note: The sequence data for this patent did not form part
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                                         Streptococcus pneumoniae DNA for cellular proliferation protein #90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trawick JD,
                                                                                  Antisense, ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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2000US-242578P.
2000US-25525P.
200US-25931P.
2001US-269308P.
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    (first entry)
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Xu HH;
                                                                                                                                                  Streptococcus pneumoniae
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26-MAY 2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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Yamamoto RT,
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  13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen
1141 TCTTCGARGACACCTGAAGAGCGTGAAAACCCAGATTTGTTAAATCCAAGCCGTCGCCGT 1200
                                                                 401 ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
                                                                                                                        421 AsnAspMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysGlyLys 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae DNA for cellular proliferation protein #361.
                                                                                                                                                                                                                             441 ArgAsnGlnMetGlnAsnMetLeuLysGlyMet------AsnLeuPro 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                              1261 AACCAGGCTAAACAGCTCATGCAGGGTGTTATGTCTGGG---
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2000US-206848P.
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2000US-257931P.
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27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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23-MAY-2000;
26-MAY-2000;
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Yamamoto RT,
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TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180
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361 TTGGCCAACAAAACAAAGAAAAAAAATGCTCGTCCTTTGATGATTGCGGCGGATATT
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Mismatches:
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Matches:
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format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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antibiotic
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                                                                                                                                                                                                                                     ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet 360
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                                            ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
                                                                                                                                          321 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
841 ACGGACATTGAAACCTTCCACCCAGACCGCATGTCTAGCCGTATCCTTGGTATGGGGGAT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE; CEG; Conserved Essential Gene; bacterial infection; antisense therapy; antibiotic resistance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---AsnLeuPro 454
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                                                                          1021 GIGCAAAATAIGGGGCCGAIGGAAGACTIGCICAAGAIGAITCCAGGIAIGGCCAACAAI
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P-PSDB; AAM01025.
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Thanassi JA;
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concoling polypeptides (AAMO1002-AAMO1114), which are essential for the viability of a bacterial cell wall. The acronym CFE stands for "CEG For Expression", where CEG stands for "Conserved Essential Gene". The nucleic acids are useful for detecting the presence of proteins essential for the viability of a bacterial cell wall in samples such as cells, tissues, biological fluids, blood, serum, nose, ear or throat swabs with ligands, and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nucleotide sequence of interest is essential for viability of a bacterial cell or whether it resides within an operon, by integrating an exogeneous nucleotide sequence comprising a portion of an open reading frame of the genomic sequence of interest (comprising 200-500 base pairs) into the genomic sequence of interest viability with a selectable phenotype to the cell, and determining cell viability with a selectable phenotype to the cell, and determining cell viability with gene therapy and antisense therapy. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids antibiotic resistant bacterial infections.

Sequence 1572 BP; 479 A; 298 C; 384 G; 411 T; 0 other;

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GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe 40
                                                                                                                                                                                                                1 MetalaPheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLySMetArgGlyLys
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          Length:
Matches:
Conservative:
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09 41 GlualaaspvalasnPheLysvalvalLysGluPheIleLysThrValSerGluArgAla

AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100 81

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541 CAAACTAATCATAACGACTATGICTTGATTGATACTGCGGGTCGTTTGCAGATTGATGAG 600 LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 181

201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220

	ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln 240             ::           ::		:::	LeuSerIleArgSerValThrGlnLysProlleLysPheValGlyMetSerGluLysLeu 280	CTGTCTGTTCGTCACATTACTGGAAAACCAATCACTTCACTGGTACAGGGTGAAAAGATT 840	AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300	ACGGACATTGAAACCITCCACCCAGACGCGIATCCTTGGTATGGGGGAT 900	ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320	:::   :::	GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340	GCTGAGAAGATGCGCGAAAACACCTTTGATTTTAATGATTTCATCGATCAATTAGATCAG 1020	VallysAsnLeuGlyProLeuAspAspIleMetLysMetlleProGlyMetAsnLysMet 360	GTGCAAAATATGGGGCCGATGGAAGACTTGCTCAAGATGATTCCAGGTATGGCAAACAAT 1080	LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlallelle 380	CCAGCCCTTCAAAACATGAAGGTGGATGAACGCCAGATTGCTCGTAAACGTGCCATTGTG 1140	GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400	TCTTCGATGACACCTGAAGAGCGTGAAACCCAGATTTGTTAAATCCAAGCCGTCGCCGT 1200	ArgilealaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420	CGTAITGCTGCTGCTTCTGGAAATACATTCGTCGAAGTCAATAAATTCATCAAGGACTTT 1260	AsnAspMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysLysGlyLys 440		ArgAsnGlnMetGlnAsnMetLeuLysGlyMetAsnLeuPro 454	GATATGAATAAAATGATGAAGCAAATGGGGGATTAATCCAAATAACCTTCCT 1350	
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Search completed: February 25, 2003, 01:52:44 Job time: 421 secs

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Alignment Scores:
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-MODEL=frame+_p2n.model -DBV=xlp
-2-Cog12003_151631_1864/app_query.fasta_1.647
-2-Cog12003_151631_1864/app_query.fasta_1.647
-2-Cog12003_15163-1864/app_query.fasta_1.647
-DB=1ssued_Patents_NA -OFWT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCH=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -TRR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-WODE-LOCAL -OUTFWT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000
-USER=USO9943108_GCGN_1_1_61_etunat_21022003_151631_1864 -NOPU=6 -ICPU=3
-NO_XLDXY -NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGIOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPPOP=6 -FGAPEXT=7
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Sequence 1958, Ap
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1722.690 Million cell updates/sec
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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
22. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                      GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                        nucleic search, using frame_plus_p2n model
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US-09-134-0010-1958
US-08-961-527-46
US-08-923-382-3
US-08-923-772-1
US-09-221-017B-928
US-09-221-017B-928
US-08-317-401E-3
US-08-317-401E-1
US-08-317-401E-1
US-08-311-401E-1
US-08-311-527A-7
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Maximum Match 100%
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GENERAL INFORMATION:
APPLICANT: Black, Michael T.
TITLE OF INVENTION: SIGNAL RECOGNITION PARTICLE POLYPEPTIDES
TITLE OF INVENTION: AND POLYNUCLEOTIDES
TITLE REPREBRUCE: GM5035
CURRENT APPLICATION NUMBER: US/09/035,382
CURRENT FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: 60/057,890
EARLIER APPLICATION NUMBER: 60/057,890
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTERQ for Windows Version 3.0
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US-09-134-001C-1980

US-08-888-207A-180

US-09-08-888-207A-180

US-08-986-963-1

US-08-96-963-3

US-09-300-682-3

US-09-309-682-3

US-09-309-682-3

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US-09-309-682-3

US-09-309-682-3

US-09-301-840A-2

US-09-103-840A-2

US-09-103-840A-1

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US-09-11-507-38

US-09-511-477-38

US-09-511-477-38

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US-08-477-831C-1


US-08-477-831C-13

US-08-477-831C-13

US-08-477-831C-13

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US-08-477-831C-13
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Matches:
Conservative:
Mismatches:
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US-09-134-001C-2243
US-09-724-517-1
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 Percent Similarity:
Best Local Similarity:
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NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1958
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Best Local Similarity:
Query Match:
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                                           GATGAATTAACGAAGTTGATGGGTGGAGAAATACATCGATTAATATGTCAAATAAACCA
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           GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT
                                                                           LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGln
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                               GlualaaspValasnPheLysValValLysGluPheIleLysThrValSerGluArgAla
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APPLICANT: Lyon Doucette-Stamm et al APPLICANT: Lyon Doucette-Stamm et al TITLE DE INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCK TITLE DE INVENTION: BPIDEMINIS FOR DIAGNOSTICS AND THERAPBUTICS

FILE REPRENCE: GTC-007

CURRENT APPLICATION NUMBER: US /09/134,001C

CURRENT FILING DATE: 1996-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                          1261 AACGATATGAAGAAATGATGAAAACAATTCACTGGTGGCGGTAAAAGGTAAAAAAGGTAAA 1320
CAGTCAATGACGCCGGCTGAAAGAAACAATCCAGACACATTGAATGTATCACGTAAAAAG 1200
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                                              Arg11eAlaLysGlySerClyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe
                                                                                                     CGTATTGCTAAAGGGTCTGGTCGTTCATTACAAGAAGTCAATCGTTTGATGAAACAATTT
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Matches:
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1958
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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynuclectides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
              180
                                                                                                          LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200
                                                                                                                                   556 AAAGAAGAACATCTAGATTTCGTTATCATTGATACAGCTGGTCGTTTACACATTGATGAA 615
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                                                                       AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
141 TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal
                                                        TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla
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APPLICATION NUMBER: US/08/961,527
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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US-08-961-527-46/c
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3033 AIGGCATITGRAAAGITTAACAGAACGITTGCAGAACGICITTAAAAAATCIACGIAAAAA 2974
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Matches:
Conservative:
Mismatches:
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TELEPHONE: (301) 309-8504
TELERAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 7577 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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74.73%
54.90%
57.43%
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Best Local Similarity:
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US-08-961-527-46
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                                                                                                2073 GCTGAGAAGATGCGCGAAAACACCTTTGATTTTAATGATTCATCGATCAATTAGATCAG 2014
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                                                                                                                                   GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
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                                                                                  ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
                                    AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09035382
Patent No. 6284515
GENERAL INFORMATION:
APPLICANT: Black, Michael T.
TITLE OF INVENTION: SIGNAL RECOGNITION PARTICLE POLYPEPTIDES
TITLE OF INVENTION: AND POLYNUCLEOTIDES
TITLE OF INVENTION: AND POLYNUCLEOTIDES
TITLE REPERENCE: GM50035
CURRENT APPLICATION NUMBER: US/09/035,382
CURRENT FILING DATE: 1998-03-05
SEARLIER RAPLICATION NUMBER: 60/057,890
EARLIER PILING DATE: 1997-09-03
NUMBER OF SEQ ID NOSS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
Conservative:
Mismatches:
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US-09-035-382-3
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                        81 AspGluLeuThrLysLeuMetGlyGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100
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GlyLysLeuThrGluAlaAspIleLysIleMetAetArgGluValArgLeuAlaLeuPhe 40
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRATSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08923772
Patent No. 297261
GENERAL INFORMATION:
APPLICANT: Black, Michael T.
TITLE OF INVENTION: NOVEL ffh
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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ZIP: 19103
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Matches:
Conservative:
Mismatches:
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             US/08/923,772
                                                                                                     NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10080
                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
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1297.00
74.51%
54.68%
57.04%
                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
CURRENT APPLICATION DATA
            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                           FILING DATE:
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Pred. No.:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO, for Win
CURRENT APPLICATION DATA:
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; Sequence 1, Application US/09385287
; Patent No. 6350857
; GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL
NUMBER OF SEQUENCES: 2
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                Length:
Matches:
APPLICATION NUMBER: US/09/385,287
FILING DATE: 30-Aug-1999
CLASSIFICATION: < Unknown>
                                                                                                                  REFERENCE/DOCKET NUMBER: GM10080
                                      APPLICATION DATA: APPLICATION NUMBER: 08/923,772
                                                                                                                                                                                                                                                              NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                           LENGTH: 1569 base pairs
                                                                 FILING DATE: <Unknown>
                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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1297.00
74.51%
54.68%
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 TOPOLOGY: linear
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                        PRIOR
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201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220
                                                                                                                                                                                                                                                                                                                                                                                                                   301 ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
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                                                                                                                                                             601 CICCICATGAAIGAGCIICGIGAIGIGGAAAGIAITGGCICAACCAAATGAAAICITGCII
                                                                              ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln
                                                                                                       LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu
                                                                                                                                                                                                                                                                         281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
                                                                                                                                                                                                                                                                                                                                                            841 ACAGATATCGAAACCTTCCACCAGACCGTATGTCTAGCCGTATCCTTGGCATGGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLECTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 ArgAsnGlnMetGlnAsnMetLeuLysGlyMet----
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; Sequence 928, Application US/092210178
; Patent No. 6444799
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 755 PAGE CITY: Palo Alto
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201. GCTCGCBAACTGGAGGAGABAATAGCCAAGABATCAGTTCGACTTCAATGACTTCCTTGC 142
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                                                            157 AspileProValTyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAla 176
                                                                                                                                                                                                                                                              GlyGlyAlaAlaLeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMet 276
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                                                                                                                                                                                                                                             GluIleMetLeuValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSer 236
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                                                                                 LeulysHisAlaLysGluGluHisLeuAspPheValIlelleAspThrAlaGlyArgLeu
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                                                                                                                                                                                                                                                                                                           PheaspaspGlnLeuaspValThrGlyValThrLeuThrLysLeuaspGlyAspThrArg
                                                                                                                                                                                                                                                                                                                          AAL INFORMATION.
APPLICANT: MUTENT, Cheryl
SETEZ, Gerald A.
COUGHLIN, Richard T.
TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377 LysAlaIleIleGlnSerMetThrPro 385
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CONNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: HALE AND DORR STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09066047A Patent No. 6306394 GENERAL INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                        CLASALICATION:
PRIOR APPLICATION ONTA:
APPLICATION NUMBER: PP1182
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
ATTORNEY/AGENT INFORMATION:
NAME: MONICOT, 614dys H
REGISTRATION NUMBER: 32,430,20021
BREGISTRATION NUMBER: 32,430,20021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: PORYPHYROMONAS GINGIVALIS
   US/09/221,017B
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1098 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 928:
SEQUENCE CHARACTERISTICS:
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1003.50
73.17%
51.49%
44.13%
                 23-DEC-1998
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   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: UNKNOWN ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
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US-09-221-017B-928
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGln 80
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,047A
FILING DATE: 24-Apr-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION OFFA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/044,869
FILING DATE: 25-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              4804
174
100
147
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Mismatches:
Indels:
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                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 106.941.156
TELECATION INFORMATION:
TELEPHONE: (617) 526-6000
INFORMATION FOR SEQ ID NO: 6:
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Matches:
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                                                                                                                                                    NAME: Superko, Colleen
REGISTRATION NUMBER: 39,850
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 4804 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                             9.27e-87
853.00
63.57%
40.37%
37.51%
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Best Local Similarity:
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APPLICANT: Taver, Debbie Sue
APPLICANT: Taver, Debbie Sue
TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE
TITLE OF INVENTION: ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59225610 NO. 5922561disk of No. 5922561th Amer
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      SOFTWARE: Petentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,401E
FILING DATE: 03-October-1994
ATCNEY/AGBNT INFORMATION:
NAME: Harrinaton
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211
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 4248.000-US TELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123 FELEPAX: 212 867 0298 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    NAME: Harrington, James J. REGISTRATION NUMBER: 38,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Aspergillus niger
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592.50
50.11%
33.84%
26.06%
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
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ADDRESSEE: No. 59225610 No. 5922561disk of No. 5922561th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 Met---AsniysMetLysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHis 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 IleLysalaileileGlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsn 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 Val------SerArgLysLysArgIleAlaLysGlySerGlyArgSerLeuGln 411
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                                             674 CAGGAAGAAGAGCTTTTCACCGAAATGACCCAGATTCAGACCGCCGTCACCCCCGACCAG 733
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                                                                                                                                                          GlyAlaAlaLeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSer 277
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                                                                                                                                                                                                                                               238 AspAspGlnLeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGly 257
                                                                                                                                                                                                                                                                                                             794 AAGGCCACCGCAGACTTCGGAGCCATCATCACCAAGACGGATGGTCACGCCGCAGGT 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            914 GAGCACCTGATGGATCTGGAACGCTTTGAGCCGAAGGCCTTCATCCAGAAGCTCCTGGGT 973
198 IleAspGluAlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGlu 217
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APPLICANT: Yaver, Debbie Sue
TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE OF
TITLE OF INVENTION: ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 GlnLeuAspGlnValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGly
                                                                                                                     218 IleMetLeuValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPhe
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US-08-317-401E-1
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               MEDIUM TYPE: Floppy disk Comparatible IBM PC comparatible OPERALING SYGEME, PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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149
71
193
17
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                              REFERENCE/DOCKET NUMBER: 4248.000-US
TELECOMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2877 base pairs
TENGTH: 2877 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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join (126..203, 253..1776)
                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,401E
FILING DATE: 03-October-1994
ATTORNET/AGENT INFORMATION:
NAME: HARTINGTON, James J.
                                                                                                                                     NAME: Harrington, James J. REGISTRATION NUMBER: 38,711
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Aspergillus niger
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573.50
51.16%
34.65%
25.22%
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
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ORIGINAL SOURCE:
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US-08-317-401E-1
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Sequence 20, Application US/08981527A

Patent No. 6410262

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: General Richard
APPLICANT: RerMano, Richard
APPLICANT: RerMano, Richard
APPLICANT: RerMano, Richard
APPLICANT: RerMano, No. 64102622e1 Secretion Factors for
TITLE OF INVENTION: Gram-Positive Microorganisms Genes Encoding Them and Methods
TITLE OF INVENTION: of USING It
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Sequence 7, Application US/08981527A Patent No. 6410262 GENERAL INFORMATION:
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430.00
53,29%
34.13%
18.91%
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Best Local Similarity:
Query Match:
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                                                                                                                                                        RESULT 12
US-08-981-527A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2351 GATTCCGTATCTCAAAAGTTTAAGGATGCCCTTGAAAAAACAAGAAACTCCTTTCAAAAC 2410
                                                                                                                                                                                                                                                                                                 2471 GAAGAGGTTCTTATCAGCGCGGATGTCGGTTTTACAACCGTTATGGAATTAATAGATGAG 2530
                                                                                                                                                                                                                                                                                                                                                                                                                       2531 CTGAAAAAAGAAGTCAAACGCAGA-----------AATATTCAAGAT 2566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2567 CCAAAGGAAGTCAAGTCAGTGATTTCTGAGAAACTGGTCGAGATTTATAACAGCGGAGAT 2626
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|TGGAAGTATGGGGAGAGCGTACAGGAGTGCCTGTCATTAAGCAGACGGCAGGAAGCGAT 2863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrasnLysLysProMetLeuValalaalaaspIleTyrargProalaalalleAsnGln 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAlaLeuSer 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 IleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeuAspGly 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluAsnThrSer---IleAsnMetSerAsnLysProProThrValValMetMetValGly 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGlnThrValGlyLysGlnIleAspIleProValTyrSerGluGlyAspGlnValLys 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProGlnGlnIleValThrAsnAlaLeuLySHisAlaLySGluGluHisLeuAspPheVal 188
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                                                                                                                                                                                                                         4 GluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLysGlyLysLeu 23
                                                                                                                                                                                                                                                                                 24 ThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPheGlu----- 41
                                                                                                                                                                                                                                                                                                                                                                                             -----LysThrValSerGluArgAlaLeuGlySerAspValMetGlnSerLeuThrPro 71
                                                                                                                                                                                                                                                                                                                                        -----AlaAspValAsnPheLysValValLysGluPheIle----
                                                                                               4370
1114
66
120
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                                                                                                                          Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                              US-09-943-108A-2 (1-455) x US-08-981-527A-20 (1-4370)
                                                                                                Length:
Matches:
                                                                                             6.96e-39
432.00
53.25%
33.73%
19.00%
                                        ORGANISM: Bacillus subtilis
                                                                                                                            Percent Similarity:
Best Local Similarity:
                                             ; ORGANISM: BAC
US-08-981-527A-20
                                                                                   Alignment Scores:
           LENGTH: 4370
SEQ ID NO 20
                             TYPE: DNA
                                                                                                                                                      Query Match:
                                                                                                Pred. No.:
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APPLICANT: Quax, Wilhelmus J.
APPLICANT: External Richard
APPLICANT: Brockhularn, Cornells P.
APPLICANT: Brockhularn, Cornells P.
TITLE OF INVENTION: No. 6410262e1 Secretion Factors for
TITLE OF INVENTION: Gram-Positive Microorganisms Genes Encoding Them and Methods
TITLE OF INVENTION: of Using It
FILE REFRENCE: GCX322-05
CURRENT FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: PCT/NL96/00278
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 20
283 LeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAspValLeu 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 GATICCGTAICTGAAAAGITTAAGGAIGGCCIIGAAAAAACAAGAAACICCTITCAAAAC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AAAGIGAAIGAICTIGIAICCCGIIACCGIAAAGIGGAIGAGGAIITCTICGAAGAGCII 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 GlyGlnGlnValIleLysIleValGlnAspGluLeuThrLysLeu-----MetGlyGly 89
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                                                                                                                                         3224 CITCAGGAATITGAICCAGAA-----TCCTAIGTGIACGGACIC-----TTITCA
                                                                                                                                                                                                                                                                            3269 GATTTAGTGGAAAAAGCCGAC-----GATTAAGAAAAAGGCCCCCAACATC 3313
                                                                                                                                                                                                                  303 SerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
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Conservative:
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OTHER INFORMATION: protein secretion chaperone US-08-981-527A-7
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1156 TATGGATTATTTGCTGATATAGAACAAAATGAAGATATTCCTGAAGAATCTCTAGA 1215
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                                                                                                                                                                                                                                                                                 628 GCTTATCGTTATCAACAAGAA---GGTAAAAAGTAATGTTAGCCGCTGGTGATACCTTC 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AsnGluIleMetLeuValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGlu 235
                                                                                       198 CAAAACTTCCAAGAACAGTTAAATTTAATTGCTCGATATAGAAAAGTTGACGAAGAT 357
                                                                                                                                                        358 TICTICGAAGCICTGGAAGAAAIG------CITATIACTGCGGACGIIGGIITIAAI 408
                                                                                                                                                                                                                                                                                                                             GluLeuThrLysLeuMetGlyGlyGlyGluAsnThrSerIleAsnMetSerAsnLysProPro 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 GluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGluAla 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 LeuGlyMet---GlyAspValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGln 314
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                                                                                                                       28 IleLysIleMetMetArgGluValArgLeuAlaLeuPheGluAlaAspValAsnPheLys 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 SerPheAspAspGlnLeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThr
                                                                                                                                                                                         48 ValValLysGluPheIleLysThrValSerGluArgAlaLeuGlySerAspValMetGln
                                                                                                                                                                                                                                                            SerLeuThrProGlyGlnGlnValIle---LysIleVal-------GlnAsp
                                                                                                                                                                                                                                                                                                                                                  122 AlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIleTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 ArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProValTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 ArgGlyGlyAlaAlaLeuSerIleArgSerValThrGlnLysProIleLysPheValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 MetSerGluLysLeuAspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIle
                                                        GluargieuGlnalaThrMetGlniysMetArgGlyLysGlyLysLeuThrGlualaAsp
                      US-09-943-108A-2 (1-455) x US-09-134-001C-1980 (1-1248)
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US-08-858-207A-180
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Sequence 1980, Application US/09134001C
Sequence 1980, Application US/09134001C
Sequence 1980, Application US/09134001C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et àl
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERALIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERBUCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR PILLING DATE: 1999-08-13
PRIOR PILLING DATE: 1997-08-14
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILLING DATE: 1997-08-14
109 LeuGlnGlyAlaGlyLysThrThrAlaGlyLysLeuAlaLeuLeuMetArgLysLys 128
                                      456
                                                                       148
                                                                                                                                   LeuGlnThrValGlyLysGlnIleAspIleProValTyrSerGluGlyAspGlnValLys 168
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                                                                                            GAAGGAAAATCTGTTGTTGCCGCGGAGACACTTTTAGAGCGGGAGCCATTGAACAG
                                                                                                                                                               517 CTGGAAGTATGGGGAGAGCGTACAGGAGTGCCTGTCATTAAGCAGGAGGGAAGCGAT
                                                                                                                                                                                                                                                                      IlelleAspThrAlaGlyArgLeuHisIleAspGluAlaLeuMetAsnGluLeuLysGlu
                                                                                                                                                                                                                                                                                                                                       ValLysGluIleAlaLys------ValLysGluIleMetLeuValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAlaLeuSer
                                   400 GIAAACGGCGTCGGGAAAACAACAACGATCGGAAAGCITGCTCATAAAATG---AAACAA
                                                                  129 TyrAsnIysIysProMetLeuValAlaAlaAspIleTyrArgProAlaAlaIleAsnGln
                                                                                                                                                                                                                                     CCGGCGCCTGTCATCTACGATGCTGTTCATGCTGCGAAAAGCAAGAAATGCCGATGTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                        757 GATGCCACGACCGGCCAAAATGCAATGGCTCAGGCAAAAGAATTCTCTAAAGCAACAAAT
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                                                                                                                                                                                                    ProGlnGlnIleValThrAsnAlaLeuLySHisAlaLySGluGluHisLeuAspPheVal
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Mismatches:
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Matches:
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Gaps:
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426.50
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31.40%
18.76%
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SEQ ID NO 1980
LENGTH: 1248
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Best Local, Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                     633 GAGGAACIGACAGCCGTTTTAGGTTCTGATACGGCAGAAATTATCAAGTCACCTAAGATT 692
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                                                                                                               693 CCAACCATCATCATGATGGTTGGTTTACAAGGGGCTGGTAAAACAACCTTGCTGGTAAA
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
STATE: Philadelphia
STATE: PA
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Mismatches:
Indels:
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APPLICATION NUMBER: US/09/007,476
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APPLICANT: Black, Michael T.
TITLE OF INVENTION: No. 6159949el FtsY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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US-09-007-476-1
; Sequence 1, Application US/09007476
; Patent No. 6159949
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COUNTRY: US
ZIP: 19103
ZORPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE

"TOTAL TENENTIER: DISKETTE

"TOTAL TENENTIER: DOS
TOTAL TE
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TELECOMONUNICATION:
TELEPHONE: 215-594-222
TELEFAX: 215-994-222
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LENGTH: 1251 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER:
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Best Local Similarity:
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US-09-007-476-1
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Mismatches:
Indels:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
FILING DATE: 14-MAY-1996
ATTORNEY AGENT INFORMATION:
                     Patent No. 6346328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Nicholas, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  AUDKESSEE: SmithKline Beecham Corporation STRRET: 709 Swedeland Road CITY: King of Prussia STATE: PA
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Matches:
Sequence 180, Application US/08858207A
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ER: P50475
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TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
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SEQUENCE CHARACTERISTICS:
LENGTH: 836 base pairs
TYPE: nucleic acid
SIRANDEDNESS: single
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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REGISTRATION NUMBER: 3
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Best Local Similarity:
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US-08-858-207A-180
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 MetLeuvalvalaspSerMetThrGlyGlnAspAlavalAsnValAlaGluSerPheAsp 238 ::::||| ::::||| ::::|||
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                                                             447
                                                                                                                                                                         125 MetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIleTyrArgProAla 144
                                                                                                                                                                                                                                                                                              145 AlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProValTyrSerGluGly 164
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685 GCTATTGATCAATTGAAAGTTTGGGGCGAACGTGTTGGTGTAAGTGTAATTAGCCAAAGT 744
                                                                                                                                                                                                                                                                                                                                                                                                                           185 LeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGluAlaLeuMetAsn 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 GluLeuLysGluValLysGluIleAlaLys-------ProAsnGluIle 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 TTTTTGAAGCTTTAGAAGAAATG-----TTAATCACTGCAGACGTCGGTTTTAAT 399
                                                                                                                88 GlyGlyGlu------AsnThrSerIleAsnMetSerAsnLysProProThrValVal 104
                                                                                                                                                                                                                 105 MetMetValGlyLeuGlnGlyAlaGlyLySThrThrThrAlaGlyLySLeuAlaLeuLeu 124
                             48 ValValLysGluPheIleLysThrValSerGluArgAlaLeuGlySerAspValMetGln 67
                                                                                           68 SerLeuThrProGlyGlnGlnValIleLysIleValGlnAspGluLeuThrLysLeuMet 87
                                                     279 LysLeuAspGlyLeuGluLeuPheHisProGluArg----
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|1222 GAAAAG 1227
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Search completed: February 25, 2003, 03:14:46 Job time : 109 secs

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Run on: ĕ

Sequence:

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APPLICANT: Dealer, KUDELL
APPLICANT: Oblsen, Kari L.
APPLICANT: 298kind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawlck, John D.
APPLICANT: Trawlck, John D.
APPLICANT: Trawlck, John D.
APPLICANT: Trawlck, John D.
APPLICANT: Trawnorto, Robert T.
APPLICANT: Trammorto, Robert T.
APPLICANT: WINGEN: John D.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: 100 PROARTY 2009/815,242
CURRENT APPLICATION NUMBER: 05/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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D US-09-070-9278.37

US-09-974-300-1847

US-09-815-242-9156

D US-09-815-242-9157

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US-09-960-352-14727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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-Gogn2_1/USPTO_spool_/US0943108/runat_21022003_151633_1953/app_query.fasta_1.647
-DB=Published_Applications_NA -QFMT=fastap -SUFFTX=rnpb -MINNATCH=0.1
-LOOPEL=0 -LOOPEXY=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR_SCORE=pct -THR_MAX=100
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-FGAPEXT=7 -YGAPOF=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 4365, Ap
Sequence 8030, Ap
Sequence 3890, Ap
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2871.303 Million cell updates/sec
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1 MAFBGLSERLQATMQKMRGK......GKKGKRNQMQNMLKGMNLPF 455
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                                                                                                                                                              February 25, 2003, 02:59:07; Search time 89 Seconds
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2: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_USB_UBB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_USB_UBB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NBW_PUB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/USO8_USB_USB_Seq:*
10: /cgn2_6/ptodata/1/pubpna/USO8_USB_USB_Seq:*
11: /cgn2_6/ptodata/1/pubpna/USO8_USB_USB_Seq:*
11: /cgn2_6/ptodata/1/pubpna/USO8_USB_USB_Seq:*
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14: /cgn2_6/ptodata/1/pubpna/USO8_USB_USB_Seq:*
14: /cgn2_6/ptodata/1/pubpna/USO8_USB_USB_Seq:*
                       GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-815-242-8090
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
Fgapop 6.0 , Fgapext 7
Pelop 6.0 , Delext
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Database :

Minimum DB : Maximum DB :

Sequence 6764, Appsequence 37, Appl Sequence 1847, Appsequence 1867, Appsequence 1868, Appsequence 1868, Appsequence 1868, Appsequence 1989, Appsequence 1985, Appsequence 2011, Appl Sequence 2011, Appsequence 1852, Appsequence 1852, Appsequence 1852, Appsequence 1851, Appsequence 2015, Appsequence 2015, Appsequence 2015, Appsequence 2015, Appsequence 2019, Appsequence 2019, Appsequence 20194,  Appsequence 201944, Appsequence 201944, Appsequence 201944, Appsequence 201944, Ap

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                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILIKO BATE: 20000112-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 8968
                                                                    TYPE: DNA ORGANISM: Staphylococcus aureus
                                                                                                                                     5.28e-245
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99.78%
99.34%
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Best Local Similarity:
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US-09-815-242-8968
                                                                                    FEATURE:
NAME/KEY: CDS
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                                                                                          LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu
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Patent No. US200200615691
Sequence 4365, Application US/09815242
Patent No. US200200615691
Sepremain Information:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Armanoto, Robert T.
APPLICANT: Armanoto, Robert T.
APPLICANT: Armanoto, Robert T.
APPLICANT: Armanoto, Robert T.
APPLICANT: ELITRA.011A
CURRENT PRILING: ILTRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-26
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
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                                                                                                                                      Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                              ength:
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEC ID NOS: 14110
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                    ; ORGANISM: Staphylococcus aureus US-09-815-242-4365
                                                                                                                           4.42e-242
2235.00
98.90%
98.24%
98.28%
                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                    Alignment Scores:
                                                    SEQ ID NO 4365
LENGTH: 1365
                                                                                  ORGANISM:
                                                                           TYPE: DNA
                                                                                                                            Pred. No.:
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                          LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu
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Patent No. US200206615691
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: APPLICANT: Zyskind, Judith W.
APPLICANT: Tawick, John D.
APPLICANT: An. H. Roward
TITLE OF INVENTION: Identification of Essent:
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/10/815
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-22
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                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8030
LENGTH: 1368
                               TYPE: DNA ORGANISM: Staphylococcus aureus
                                                                                                               4.44e-242
2235.00
98.90%
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                                                            ; NAME/KEY: CDS
; LOCATION: (1)...(1368)
US-09-815-242-8030
                                                                                                                                             Best Local Similarity:
                                                                                                                           Score:
Percent Similarity:
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                         TTATCTATTCGTTCGGTGACAAAAAACCAATTAAATTTGTTGGTATGAGTGAAAGTTA
                                                                                                 ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu
                                                                                                                                                                                              GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln
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1321 CGCAATCAAATGCAAAATATGTTAAAAGGTATGAATTTACCGTTT 1365
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APPLICANT: CART, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essentificate of INVENTION: Identification of Essentificate REPERENCE: ELITEA.OIL
FILE REPERENCE: ELITEA.OIL
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 00/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLICATION NUMBER: 60/257,931
PRIOR PLICATION NUMBER: 60/257,931
PRIOR PLICATION NUMBER: 60/269,308
PRIOR PLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-16
NUMBER OF SED ID NOS: 14110
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APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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481 TITGATATGGGAACAGATGCTAATCCAGTGGAAATTGTTCGTCAAGGGTTAGCATTAGCA
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                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                         Matches:
                                                                               Length:
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                      TYPE: DNA ORGANISM: Enterococcus faecalis
                                                                          3.17e-150
1418.50
77.54%
58.96%
62.38%
                                                                                                  Percent Similarity:
Best Local Similarity:
                                            US-09-815-242-3890
                                                                   Alignment Scores:
           1416
SEQ ID NO 3890
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341 ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet
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FILE REPERENCE: ELITAR.011A
CURRENT APPLICATION NUMBER: U5/09/815,242
CURRENT FILING DATE: 2001.03-21
PRIOR PILING DATE: 2000.03-21
PRIOR PILING DATE: 2000.05-23
PRIOR PILING DATE: 2000.05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/203,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000.11-27
PRIOR PILING DATE: 2000.11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/263,838
PRIOR APPLICATION NUMBER: 60/263,838
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                              TYPE: DNA ORGANISM: Enterococcus faecalis
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1418.50
77.54%
58.96%
62.38%
                                                                                       ...(1434)
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Best Local Similarity:
                                                                                        ; LOCATION: (1).
US-09-815-242-6764
                                                                          NAME/KEY: CDS
                                                                                                                                     Alignment Scores:
SEQ ID NO 6764
LENGIH: 1434
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                                                             FEATURE:
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TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982 CORRESPONDENCE ADDRESS:
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CIGICAATICGGGCAGIAACGGGCGCICCGATIAAAIITIGICGGTICTGGIGAAAAAIIA 840
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                                                                            841 ACCGATTAGAAATTTTCCATCCCGATCGTATGTCGAGTGTATGTCGAGTGTATGGGGGAC
                                             AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra MSDOS version 6.2
SOFRWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AsnAspMetLysLysMetMetLysGlnPheThr-----
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FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Charles A. Kunsch
Patrick J. Dillon
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COUNTRY: USA
ZIP: 20850
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US-09-070-927A-37
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4682 GCTCAAAAATGAAAGAAAACAGTTTTGACTTTAACGATTTCATTGAGCAATTGGATCAA 4741
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                                                                                                                                                                                                                                                                                                                                                          4622 ATGTTGACGCTAATTGAAAAAGCGCAACAAGATTACGATGAGAAAAAAGCAGAAGAACTT 4681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
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                                                              241 LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla
                                                                                                     261 LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu
                                                                                                                                                                                                                                 281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
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                                                                                                                                                                                                                                                                                                                                                                                                   321 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln
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APPLICANT: Clausen, ID Groth
TILLE OF INVENTION: Methods For Monitoring Multiple Gene
TILLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2000-10-06
PRIOR PLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 AsnAspMetLysLysMetMetLysGlnPheThr-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1847, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Wind
SEQ ID NO 1847
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US-09-974-300-1847
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                   REFERENCE/DOCKET NUMBER: PB369
APPLICATION NUMBER: 60/066,009
                                                          NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 6729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                 FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
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1417.50
77.54%
58.96%
62.34%
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Best Local Similarity:
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  ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet 360
                                                                GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln
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APPLICANT: OILSEN, MAIL M.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramenoto, Robert T.
APPLICANT: Xamemoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: DEPOSITY OF SERVICES.
FILE REPERBRUGE: ELITRA.011.07
FURENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00/201,078
FRIOR FILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-12-22
FRIOR FILING DATE: 2000-12-22
FRIOR FILING DATE: 2000-12-22
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FRIOR FILING DATE: 2000-12-22
FRIOR FILING DATE: 2000-12-22
FRIOR FILING DATE: 2001-02-24
FRIOR FILING DATE: 2001-02-24
FRIOR FILING DATE: 2001-02-25
FRIOR FILING DATE: 2001-02-26
FRIOR FILING DATE: 2001-02-26
FRIOR FILING DATE: 2001-02-26
FRIOR FILING DATE: 2001-02-3
FRIOR FILING DATE: 2001-02-26
FRIOR FILING DATE: 2001-02-3
FRIOR FILING DATE: 2001-02-3
FRIOR FILING DATE: 2001-02-3
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                              Sequence 9156, Application US/09815242 Patent No. US20020061569a1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Streptococcus pneumoniae
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Zyskind, Judith W.
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US-09-815-242-9156
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401	Db 1201 CGTATTGCTGCTC Qy 421 ASNASpMetLySI	⊣	NY 441 AIGASHG-LIMBEC   Db 1300GATATGA	RESULT 10 US-09-814-041A-1 ; Sequence 1, Applic, ; Patent No. US20020	; GENERAL INFORMATION: ; APPLICANT: CHEBVER, ; APPLICANT: FEOTEAU ; APPLICANT: LI, HU	APPLICANT: PAYNE , APPLICANT: STEEL , APPLICANT: WANG, , TITLE OF INVENTIO	; TITLE OF INVENTIO ; FILE REFERENCE: G ; CURRENT APPLICATION ; CURRENT FILING DAV	PRIOR APPLICATION PRIOR PILING DATE NUMBER OF SEQ ID SOFTWARE: FastSEQ	; SEQ ID NO 1 ; LENGTH: 1569 ; TYPE: DNA ; ORGANISM: Streptocc	Alignment Scores: Pred. No.:	Socie: Percent Similarity: Best Local Similarity Query Match:	-09-94	OY I MerklaPheGlud	Qy 21 GlyLysLeuThrC       ::::    Db 61 GGAAAATCTCTCT	Qy 41			Qy 101 ProThrvalvalv
		GTCGGCATGAGGTCATTGATACATTGATAATCCTGCGCAACAGATTATAAATCGTTGAT	AspGluLeuThrLysLeuWetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100 :::	ProthryalyalMetWetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLys 120 	LeualaLeuLeumetargLysLysTyrasnLysTysProMetLeuvalalaalaaspile 140           TIGGCCAACAAACTCAAGAAAAGAGAAATGCTCGTCCTTTGATGATGGGGGGGATATT 420	TyrargproalaalaileasnGlnLeuGlnThrValGlyLysGlnIleaspIleProVal 160 	TyrsergluglyaspglnValLysProglnglnIleValThrAsnAlaLeuLysHisAla 180:	LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200 :::	. AlaLeuWetAsnGluLeuLysGluValLysGluIlealaLysProAsnGluIleMetLeu 220 	ValvalAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln 240 	LeuaspvalthrGlyvalthrLeuthrLysLeuaspGlyaspthrargGlyGlyalaala 260     :::	LeuSerllehrgSerValThrGlnLysProlleLysPheValGlyMetSerGluLysLeu 280	AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300 :::	ValLeuSerLeurleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320 :::   :::	GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGluGlnLeuAspGln 340 :::	Vallysksnleuglyproleuaspaspilemetlysmetileproglymetasnlysmet 360	. LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIle 380	GINSEIMETTHEFROALAGIUARGASDASDPROASPTHELEUASDVALSERARGLYSLYS 400
Db 61 Qy 41	Db 121	1	Qy 81 Db 241	Qy 101 Db 301	Qy 121 Db 361	Oy 141 Db 421	Oy 161 TDb 481	Qy 181 Db 541	Qy 201 Db 601	Oy 221 Db 661	Oy 241 Db 721	Qy 261 Db 781	Qy 281 Db 841	QY 301 Db 901	Qy 321 Db 961	Qy 341 Db 1021	OY 361 Db 1081	Qy 381

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: METHODS USING THE SRP POLYNUCLEOTIDES : AND POLYPEPTIDES COMPOUNDS MODULATING THEIR ACTIVITY 50069
                GlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
                                               SLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysLysGlyLys 440
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LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle 140
                         361 TIGGCCAACAAACTCAAGAAGAAGAAAATGCTCGTCCTTTGATGATTGCGGCGGTATT 420
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                                                                           421 TATCGTCCAGCTGCCATTGACCTTAAGACCTTGGGACAACAGATTGATGTGCCTCTC 480
                                                                                                        TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180
                                                                                                                                  481 TIMGCACTIGGAACAGAAGIACCAGCIGITGAGAITGIACGICAAGGITIGGAGCAAGCC 540
                                                                                                                                                             LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200
                                                                                                                                                                            AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220
                                                                                                                                                                                                                                   ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln 240
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Publication No. US20020197605A1
GENERAL INFORMATION:
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Matches:
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CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                          TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1900-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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OCHIAI, KEIKO
NAKAGAWA, SATOSHI
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TATEISHI, NAOKO
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IKEDA, MASATO
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
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                                                                                                                                                              TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: PROKARYOTES
TITLE OF INVENTION: PROKARYOTES
TITLE OF INVENTION: PROKARYOTES
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-010-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
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71.74%
50.99%
51.21%
                                                                                                                                      Yamamoto, Robert T.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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US-09-815-242-6166
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                                                                                                                            APPLICANT:
APPLICANT:
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                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1264 GACATGCAGCGCATGATGAAG-------AAAATGAAGAAGGGCGGAATG 1305
                                                                                                                                                                                                                                                                                                                                 263 IleArgSerValThrGlnLysProlleLysPheValGlyMetSerGluLysLeuAspGly 282
                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAspValLeu 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysMetArgGlu---SerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGlnVal 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 GlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIleGln 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLysArg 401
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ProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProValTyrSer 162
                                                                                                                         GluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGluAlaLeu 202
                                                                                                                                                                                                                                                  223 AspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeuAsp 242
                                                                                                                                                                                                                                                                               664 GACGCCATGACCGGTCAGGATGCGGCCAATACGGCAAAAGCATTCAATGAAGCGTTACCG 723
                                                                                                                                                                                                                                                                                                                                                                                                         784 ATTCGTCACATCACTGGCAAACCGATCAAGTTCCTCGGTGTTGGCGAGAAAACTGAGGCG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeuGluLys 322
                MetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeuValVal
                                                                                                                                                                                                         ValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAlaLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMetLys
                                                            163 GluGlyAspGlnValLySProGlnGlnIleValThrAsnAlaLeuLySHisAlaLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1949, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
APPLICANT: Wall, Daniel
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GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe 40
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Matches:
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                                                                  of Essential
                          APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essent.
TITLE OF INVENTION: Identification of Essent.
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-10-33
PRIOR FILING DATE: 2000-10-33
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14110
SCOFWARE: FaatSEQ for Windows Version 4.0
SEQ ID NO 1949
LENGTH: 721
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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               Carr, Grant J.
Yamamoto, Robert T.
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1158.00
99.58%
98.73%
50.92%
Trawick, John D.
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Best Local Similarity:
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23 LeuThrGluAlaAspIleLysIleMetArgGluValArgLeuAlaLeuPheGluAla 42
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                                                       LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200
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                3 PheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgClyLysGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPhe 237
                                                                                                                                                                                        APPLICANT: Oblisen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Camamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Referification of Essential Genes in FILE REFERENCE: ELITRA.0118
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Mismatches:
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Matches:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTHRRE: FASTEED for Windows Version 4.0
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Gaps:
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APPLICANT: Haselbeck, Robert
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US-09-815-242-7850
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                                                                                                                                                                                                                                              US-09-815-242-7850
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103 ValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrThrAlaGlyLysLeuAla 122
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                                                                                                                                                                                                      63 SerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGlnAspGlu
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    184 GAAGAAGTCAATAAAAGTTTAACGCCAGGGCAAGAATTCTTAAAAATCGTTCAGCGTGAG 243
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                                                                                                  223 AspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeuAsp
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APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant J.
APPLICANT: Trawick, John D.
APPLICANT: Yamanoro, Robert T.
APPLICANT: Yamanoro, Robert T.
APPLICANT: Wall H. Boward
TITLE OF INVENTION: Incorp.
TITLE OF INVENTION: Prockaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
FRIOR APPLICATION NUMBER: 60/201,078
FRIOR RPLING DATE: 2000-05-21
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-23
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APPLICANT: Ohlson, Kari L.
APPLICANT: Yashind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Travick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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16154066 seqs, 8097743376 residues

Searched:

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Database :

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GSS 01-MAY-2002 LLMGtag644 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, DNA sequence.
BH770912
BH770912.1 GI:20373869
GSS. Lactococcus lactis subsp. cremoris. Lactococcus lactis subsp. cremoris Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.

1 (bases 1 to 2169)

Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis RESULT 1 BH770912/c LOCUS DEFINITION ORGANISM ACCESSION VERSION AUTHORS TITLE KEYWORDS SOURCE REFERENCE

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                                                                                                                                                                                                        /strain="MG1363"
/db_zrei="taxon:1359"
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/clone_lib="MG1363 Random Sequence Tag Library"
/note="vector: pSGMU2; Site_l: Smal; Library of
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best homologue in strain IL1403
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AF075878 Salmonella typhimurium LT2, Lambda DASH II Salmonella typhimurium genomic clone 245-T3, DNA sequence.
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GlyMetSerGluLysLeuAspGlyLeuGluLeuPheHisProGluArgMetAlaSerArg
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Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego,
Email: mcclelland@lifsci.sdsu.edu
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/clone="245-T3"
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1 (bases 1 to 875)
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MEDLINE
COMMENT
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Query Match:
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ORIGIN
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JOURNAL
                                                                                                                                                          REFERENCE
RESULT 3
BI934118
                                                       ACCESSION
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KEYWORDS
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| ATGGGCBARGAGACAGACGAGATTTTAC-TCGCAGCCGCGCGTAGTATGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  87 MetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysProProThrValValMetMet
                                                                                                                                                                                           107 ValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLysLeuAlaLeuLeuMetArg
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152
57
76
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                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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757.50
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53.15%
33.31%
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Best Local Similarity:
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 178
                                    Scores:
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EST 18-0CT-2001
                                                                                                                                                               Lycopersicon esculentum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then states-separated while remaining frozen."
                                                                                                                                                                                                                                                                              Tases 1 to 773)

van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J., Utterback, T., Van Aken, S., Roning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J., and Tanksley, S.D. Generation of ESTs from tomato flower tissue, anthesis (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysProProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrAla 118
B1934118 773 bp mRNA linear EST 18-OCT EST54007 tomato flower, anthesis Lycopersicon esculentum cDNA
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134
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63
1
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/clone_lib="tomato flower, anthesis"
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Matches:
Conservative:
Mismatches:
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Clemson University Genomics Institute
                                                   clone cTOD18J16 5' end, mRNA sequence.
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Gaps:
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Location/Qualiflers

1. .73

organism="Lycopersion es/cultivar="TA496"

/db_xref="taxon:4081"
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/dev_stage="anthesis"
                                                                       BI934118
BI934118.1 GI:16248590
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715.50
75.19%
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31.46%
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FOORI; Plants were grown under six following different environmental regimes in greenhouse, Environment; 240c/170c day/night, well-watered, with post-anthesis fertilizer. Environment 2) 240c/170c day/night, well-watered, with post-anthesis fertilizer, Environment 3) 370c/170c day/night, well-watered, with post-anthesis fertilizer, Environment 4) 370c/170c day/night, well-watered, with post-anthesis fertilizer, Environment 5) 370c/170c day/night, well-watered, with post-anthesis fertilizer, Environment 5) 370c/170c day/night plus drought, with post-anthesis fertilizer, Environment 6) 370c/170c day/night plus drought, without post-anthesis fertilizer, day/night plus drought, without post-anthesis fertilizer, day/night plus drought, without post-anthesis fertilizer, day/night plus drought, without post-anthesis fertilizer, day/night plus drought, without post-anthesis fertilizer, and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 35, 7, 8, 10, 12, 16, 20, 24, 28, 35, 7, 8, 10, 12, 16, 20, 24, 28, 35, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A CDNA library was made using poly (A) RNA, and the cDNA clones were in vivo excised to give pBluescript SK(-) phagemids in the TV Close lab (Chin, Close, Fenton) at the University of California, Riverside Enland DNA environment 4, physical DNA environment 4, physical DNA environment 4, physical DNA environment 4, physical DNA environment 5, physical DNA environment 6, physical DNA en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 TACTCAGAAGGAACCGCGGCCAAACCTGCAGAATAACCAAGAATGCCGTGGAAGAGGCG
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                     Adev stage="3.44 days post anthesis seed"
Alab_host="E. coli SOLR"
Anote="Vector: Lambda ZAP II, excised phagemid;
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115 c 179 g
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27.75%
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
1 (bases 1 to 656)
Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J., Cronin,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J.,
Wilson,C. and Woo,J.
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomes - Developing grains cDNA library
Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspileTyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspile 158
                                                                                                                                                                                                                                                                          HisAlaLysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIle 198
                                                                                                                                                                                                                                                                                                                                                                                              AspGluAlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIle 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   598 CTCGAAATTGGGATTACTGGTGCCATCTTGACGAAGCTAGATGGAATTCTAGGGGTGGA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaAlaLeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGlu 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyLysLeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAla 138
                                                        241 GCAAAGTTAGCTTTATATCTA---AAGAAGCAGGGTAAGAGTTGCATGCTGATTGCTGGA 297
                                                                                                                                                                               GACGIGIACAGACCIGCIGCIATIGACCAACTIGITATITIGGGTAAACAGGTIGATGTA 357
                                                                                                                                                                                                                                           ProValTyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLys 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 MetLeuValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAsp 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum aestivum"
/cultivar="Butte 86"
/db_xaron:465"
/db_xaron:4566_H12_P24"
/clone="WHE3566_H12_P24"
/clone=lib="Wheat developing grains cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 AspGlnLeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysLeuAspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeu 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTATGGAGGACCTTGAACCTTCTATCTGACCGCATGGCTGGACGTATTTA 771
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BQ805434.1 GI:22029643
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Fax: 5105595818
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COMMENT

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AK011928

Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610209c12:signal recognition particle 54 kR0, full insert sequence.

AK011928

AK011928-1 GI:12848353

HTC; CAP trapper.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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                                                                                                                                                                                                                                                                                                                                      469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 rglysLysArgileAlaLysGlySerGlyArgSerLeuGlnGlu-ValAsnArgLeuMet 417
                                                                                                            649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2610209C12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 uLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGlnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 GAAAGAGAAGAATAGCTAAAGGTTCTGGTACAACAGTACAAGAAGNTAAATAAAGTTCTT
                                                                                                                                                                                                                                                                                                                        uSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeuAs
                                                                                                                                                                                                                         242 AspvalThr-GlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAlaLe
                                                                                                                                                                                                                                                  LeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeuVal
                                                                                                                                                 ValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeu
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
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51 AAAAGGCTATGAAATGATGAAAAGCAAATGAAGCAA 15
                                  US-09-943-108A-2 (1-455) x BF940797 (1-711)
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                                                                                                                                                                                                                                                                                     711 bp mRNA linear EST 22-JAN-2001 MAGE: 3289406. X Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE: 3280811 3' similar to SW:SR54_BACSU P37105 SIGNAL RECOGNITION BP940797 ROTEIN ;, mRNA sequence. BF940797.1 GI:12358117 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Lupski Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 433.
Location/Qualifiers
1. 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pcwv-SPORT6 (Life Technologies); Site_1:
Not1: Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5.7cGACCAGCGGGTCG-3' and
5'-GACTAGTTCTAGATGGGGGGGGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 711)
MOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                           542
                   482
                                                        ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
                                                                                                                                GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
                                                                                                                                                                     543 CAGAAGAAGATCATGAGTGCGAAATTTGACTTCAATGACTTTTTAAAGCAGACACAAAAT 602
483 GICCTITCATITGITGAAAAAGCACAAAAGICGITCGCCAAGAGAGATACCATGGAACTG
                                                                                                                                                                                                                                 341 ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsn 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Lupski_dorsal_root_ganglion"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                711
134
48
45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lupski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:3280811"
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AUTHORS
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QFQNIMMKOGPRQILGMIPGFGTDPWSKGNEDGESMALKKTMINDSMDDELDSTDG
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NIKLVKQLRENVKSAIDLEEMASGLNKRKMIQHAVFKELVKLVDPGVKAWTPIKGKQN
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GSYTEMDPVIIASEGVEKFKNENFEIIIVDTSGRHKQEDSLFEEMLQVSNAIQPDNIV
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                                                                                                                                                            /clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LeullaleuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598 TTAGCATATTATTACCAGAGGAAA----GGTTGGAAGACCTGTTTGATATGTGCAGATACA 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetalaPheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe
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                                                                                                                                                                                                                                                                                    238. .1752
/gene="Srp54"
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                                 /db_xref="FANTOM_DB:2610209C12"
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                                                            /db_xref="MGD:MGI:1905318"
/db_xref="taxon:10090"
                                                                                                                                                                                    /dev_stage="10 days embryo"
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/db_xref="GI:12848354"
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S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Bronstein, M., Bult, C., Arakawa, T., Baldaralli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Huncha, J., Inordani, Y., Isohi, Y., Isohi, Y., Isohi, M., Tawam, M., Kasaikawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Nouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Sakai, K., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tagama, M., Tagawa, A., Takahashi, F., Tagama, M., Tagawa, A., Takahashi, F., Tagami, M., Tagawa, A., Takahashi, F., Tagami, M., Tagawa, A., Takahashi, F., Tagami, M., Muramatsu, M., and Hayashizaki, Y., Yoshida, K., Yoshido, M., Muramatsu, M., and
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                                                                                                                                  genes
                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Karbana, T., Nashiro, H., Itoh, M., Skonno, H., Akiyama, J., Nishi, K., Itana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Matsumoto, H., Sakaguchi, S., Ikegami, T., Rashiwagi, K., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yeljawak, S., Inoue, K., Tagawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tawaka, T., Watsunra, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKBN Integrated sequence analysis (RISA) system--884-format sequencing pipeline with 384 multicapillary sequencer
                          Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNas to prepare full-length cDNa libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Nature 409 (6821), 685-690 (2001)
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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/organism="Mus musculus"
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ORGANISM Anopheles gambiae  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  Anopheles  Anopheles  I (bases 1 to 688)  AUTHOR  Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.  TITLE  Direct Submission of BAC-end sequences from Anopheles gambiae  JOURNAL  Other_GSSS: AG-ND-13B11.TR  COMMENT  Contact: Brendan J Loftus  Department of Eukaryotic Genomics  The Institute for Genomic Research  9712 Medical Center Dr., Rockville, MD 20850, USA  Tel: 301 838 0208	Fax: 301 B88 354 Fax: 301 B88 354 Fax: 301 B88 354 Fax: 301 B88 354 Fax: 301 B88 354 Fax: 301 B88 354 Fax: 301 B88 354 Fax: 301 B88 554 Fax: 302 B88 554 Fax: 3	/Grail=Texon:7165" /Glone="AG-ND-138B11" /Glone=11b="ND-TAM" /Glone=11b="ND-TAM" /Glone=11b="ND-TAM" /Glone=11b="ND-TAM" /Glone=11b="ND-TAM" /Glone=11b="ND-TAM" /Glone=11b="ND-TAM" /Glone=11b="ND-TAM" /Glone=11b="ND-TAM" /Glone=11b=		QY 100 ProprothrvalvalMetMetValGlyLeuGlnGlyAlaGlyLySThrThrAlaGly 119	09 140 IleTyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIlePro 159  11
R	954 260 1014 280 1074 300 1134 FEATU	uAsp 339  TCAG 1248  n 358  CACA 1308  SILe 376  :::	411 1482 429 1542	ysLysGlyLysArgAsnGlnMet 444     ::::::          ::::::           ::::::           ::::::	688 bp DNA linear GSS 11-DEC-2001 nopheles gambiae genomic clone AG-ND-138B11
161 715 181 775 201 835	895 241 955 261 1015 281 1075	OY 320 LeuGluLysLysMetargGluSe.  OY 320 LeuGluLysLysMetargGluSe.	OY 397SerArgLy Db 1423 TTCAGTAAGCAACCAGGGAGAAT QY 412 GluValAsnArgLeuMetLySGl :::    Db 1483 GATGTTCAAGAACTTCTGACCCA	Oy 430	RESULT 7 BH394904 LOCUS DEFINITION AG-ND-138B11.TF ND-TAM AGCESSION BH394904 ACCESSION BH394904.1 GI:17341045 KEYMORDS SOURCE African malaria mosquito

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Query Match: 24.74% Indels: 1 DB: 10 Gaps: 1		2 TTGATTCGAGGTGTAAAACCAGATCAGCAACTAGTTAAGACTGTACGTGACGAGCTTGTG 85 LysLeuwetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysFroProThrValVal	Db 62 AAACTGATGGGTGGAGAGGTTTCTGAACTGGTTTTTGCTAAATCTAAGCCCACCGTAATA 121  Qy 105 MetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLysLeuAlaLeuLeu 124  :::::	125 MetArgLysLysTyrAsnLysLysProMetLeuValAlaalaaspIleTyrArgProAla :::	145 ASDGINGALGENGINING AGG TO THE SET THE STORE STORE AGG TO THE STORE STORE AGG TO THE AGG TO THE STORE AGG	DD 299 ACAGAIGIANAANCLIGCAGAAIAAGCUCGAGAGAGAITACAAGAGGCUCAAAAAGAAI 358 QY 185 LeukspPheValilelleAspThralaGlyArgleuHisIleAspGlualaLeuMetAsn 204 :::	QY 205 GluLeuLysGluValLysGluIlealaLysProAsnGluIleMetLeuValValAspSer 224	Qy 225 MetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeuAspValThr 244	Qy 245 GlyvalThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAlaLeuSerIleArg 264	593 bp mRNA seedlings,	sequence.	Septractopy, Asteridae, euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.  Lycopersicon.  REPERENCE I (bases I to 53), White, R., van der Hoeven, R.S., Holt, I.E., Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, R., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M., Remman, W., Fraser, C.M., Glovannoni, J.J., Martin, G.B. and Tanksley	TITLE 'S-L. 'S-L. 'Generation of ESTs from germinating tomato seed JOURNAL Unpublished (2000) COMMENT Contact: CUGI Clemson University Genomics Institute Clemson University
	199 pGluAlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGlu-IleM	219 etLeuValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspA	Oy 239 spGlnLeuAsp-ValThrGlyValThrLeuThrLysLeuAspGlyAspThrArg-GlyGl 258.	Db 599 GGCCGGCATAACAATCCGTTCCGGTAGTAAAAACCAATTAAGTTAATTTCTACCGGT 658  Qy 278 GluLysLeuAspGlyLeuGluLeuPhe 286  Dh 659 GACAAAAACCAACAAAACAAAAAAAAAAAAAAAAAAAA	SULT 8 432304 SUS FINITION		UNGANISM LYCOPERSIGNON SECURENCES STREPTOPHYTA; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Trachericae	<pre>Lycopersicou. ATHORS 1 (bases 1 to 605) ATHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley</pre>	,S.D. TITLE ,S.D. TITLE Generation of ESTs from tomato fruit tissue, breaker stage JOURNAL Unpublished (2000) COMMENT Contact: CIGI	urce	/Oultrvar="14496" /db_xref="taxon:4081" /clone="clEG7M2" /clone=lih="tomato breaker fruit, TIGR" /tissue_type="Pericarp" /dev_stage="breaker" /lab_host="solars" /lab_host="solars"	Another Petton:piusocliptosmodadapi,strei = COSMI,strei = Natei	Alignment Scores: 3.86e-52 Length: 605 Score: 562.50 Matches: 105 Percent Similarity: 75.25% Conservative: 47 Best Local Similarity: 51.98% Mismatches: 49

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade, Panicoideae; Andropogoneae; Zea.
496035E06.x1 496 - stressed shoot cDNA library from Wang/Bohnert lab Zea mays cDNA, mRNA sequence.
A1977909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 AsnLysProProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrThr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 AlaGlyLysLeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAla 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 AlaAspileTyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAsp 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 IleProValTyrSerGluGlyAspGlnValLySProGlnGlnIleValThrAsnAlaLeu 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="salt stress"
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Wang/Bohnert"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4577"
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Wang/Bohnert lab"
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Maize ESTs from various cDNA libraries sequenced at
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105
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Department of Biological Sciences
Stanford University
S5 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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Plate: 496035 row: E column:
Location/Qualifiers
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/organism="Zea mays"
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                                                  AI977909.1 GI:5791117
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555.50
74.61%
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                                                                               /organism="Lycopersicon esculentum"
/cultivar="TA496"
/cultivar=TA496"
/cultivar=TA496"
/cultivar=TA496"
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91 a 97 c 159 g 146 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 LysProGlnGlnIleValThrAsnAlaLeuLysHisAlaLysGluGluHisLeuAspPhe 187
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     100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 SerPheThrLeuAspAspPheLeuGluGlnLeuAspGlnValLysAsnLeu 344
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                                                                                                                                                                                                                                                                                                                                                                                                           272 LysPheValGlyMetSerGluLysLeuAspGlyLeuGluLeuPheHisProGluArgMet 291
                                                                            172 IleValThrAsnAlaLeuLySHisAlaLySGluGluHisLeuAspPheValIleIleAsp 191
                                                                                                                                                                                                                                                          292 AlaSerArgIleLeuGly-MetGlyAspValLeuSerLeuIleGluLysAlaGlnGlnAs 311
152 ValGlyLysGlnIleAspIleProValTyrSerGluGlyAspGlnValLysProGlnGln 171
                                                                                                                                                        192 ThralaGlyArgLeuHisIleAspGluAlaLeuMetAsnGluLeuLysGluValLysGlu 211
                                                                                                                                                                                                                                                                                                                                                 332 GCTTTGGTCACAACATTCAATCTCGAAATTGGAATTACTGGTGCCATCTTGACGAAGCTA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 pValAspGlnGluLysAlaLysAspLeuGluLysLysMetArgGluSerSerPheThrLe 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          572 TATGCGTCAAGAAGATGCTGAAGAATTGCAGAAGAAGATCATGAGTGCAAAATTTGATTT 631
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Library"
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public
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                      212 IlealaLysProAsnGluIleMetLeuValValAspSerMetThrGlyGlnAspAlaVal
                                                                                                                                                                                                                                                                                                                                                                                       252 AspGlyAspThrArgGlyGlyAlaAlaLeuSerIleArgSerValThrGlnLysProIle
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Submitted (25-APR-2002) Maize Mapping Project, University Missouri, Columbia, MO 65211, USA
Missouri, Location/Qualifiers
1. .1200
/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="this sequence is part of a project of assemblies resulting from the application of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="PC0070230"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Overgo Probes
Unpublished (2002)
2 (bases 1 to 1200)
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Zea mays
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JOURNAL
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                                                                                                                                                                                                                                                                                                                               BM413418 677 bp mRNA linear EST 22-JAN-2002 EST587745 tomato breaker fruit Lycopersicon esculentum cDNA clone cLEG63C14 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescriptskmCJadapt; Site_1: EcoRl; Site_2: XhoI; supplier: Boyce Thompson Institute; Sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tse, J. Bougri, O., Kirkness, B., Utterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of ESTs from tomato fruit tissue, breaker stage (2002) Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                          LysHisAlaLysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHis 197
                                                                                  198 IleAspGluAlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGlu 217
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101
46
47
1
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/oultivax="TA466"
/db_xref="taxon:4081"
/clone="cLEG63c14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="tomato breaker fruit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                      218 IleMetLeuValValAspSerMetThrGlyGlnAspAla 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
Gaps:
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/dev_stage="breaker"
/lab_host="SOLR"
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1. .677
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534.00
75.38%
51.79%
13.48%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   tomato.
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DB:
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BM413418
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DEFINITION
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1 (bases 1 to 533)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
Unpublished (1999)
                       Lycopersicon esculentum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /_note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; CLEF - Fruit were tagged at the 1cm stage and harvested 3-5 days prior to ripening. Fruit were cut in harl to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 LysTyrAsnLysLysProMetLeuValAlaAlaAsplleTyrArgProAlaAlaIleAsn 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnLeuGlnThrValGlyLySGlnIleAspIleProValTyrSerGluGlyAspGlnVal 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 AAGCAGGGTAAGAGTTGCATGCTGAAGACGTGTACAGACCTGCTGCTATTGAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValileileAspThrAlaGlyArgLeuHisIleAspGluAlaLeuMetAsnGluLeuLys 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeuAspValThrGlyValThr 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluvalLysGluIleAlaLysProAsnGluIleMetLeuValValAspSerMetThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 LysProGlnGlnIleValThrAsnAlaLeuLysHisAlaLysGluGluHisLeuAspPhe
                                                                                                                                                                                                                                                                                                                                               /organism="Lycopersicon esculentum"
/cultivar="TA406"
/db_xref="Laxon.4081"
/clone="cleB40N15"
/clone_lib="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/lab_type="fruit green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                             Clemson University Genomics Institute
Clemson University
100 Jozdan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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97
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Conservative:
Mismatches:
Indels:
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513.50
76.27%
54.80%
22.58%
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1 86 c
                                                                                                                                                                                                                                                                                                 prime sequence.
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                                                                                            Lycopersicon.
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Best Local Similarity:
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COMMENT
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                                                                                                            REFERENCE
                                                                                                                           AUTHORS
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contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."

1 216 c 317 g 279 t l others
                                                                                                                                                                                                                                                                                                                                                                                             71 CAAGAAGCAGCAGCACTAGTCACCACCTTCAATATTGAGATTGGTATAACTGGTGCAATA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 AlaGlnGlnAspValAspGlnGluLysAlaLysAspLeuGluLysLysMetArgGluSer 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 SerPheThrLeuAspAspPheLeuGluGlnLeuAspGlnValLysAsnLeuGlyProLeu 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 AAATTCGACTTCAACGATTTCTTAAAACAATCTCAAAAGGTTGCGAAAATGGGGTTCCATG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 AGCCGCATTATTGGAATGATGCCAGGCATGAACAAGATAACTCCCGCA---CAAATCCGA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 MetSerGluLysGlnIleAspHisIleLysAlaIleIleGlnSerMetThrProAlaGlu 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 ArgAsnAsnProAspThrLeuAsnValSerArgLysLysArgIle-----AlaLysGly 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406 SerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPheAsnAspMetLysLys 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 GluValLysGluIleAlaLysProAsnGluIleMetLeuValValAspSerMetThrGly 227
                                                                                                                                                                                                                                                                                                                                                                   GlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeuAspValThrGlyValThr 247
                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAlaLeuSerIleArgSerValThr 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 CTGACTAAATTGGATGGTGACTCCAGGGGCGGAGCCGCACTAAGCGGTTAAAGAGGTCTCT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProGluArgMetAlaSerArgIleLeuGlyMetGlyAspValLeuSerLeuIleGluLys 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 AspAspIleMetLysMetIleProGlyMetAsnLysMetLysGlyLeuAspLysLeuAsn 367
                                                                                                                                                                                                                                                                                                                                  70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 GAAGTGAAGAAGGCTGTTAATCCTACAGAAGTTCTGCGTTGTCGTGGCCATGACTGCC
                                                                                                                                         1200
102
63
65
3
                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            668 CAGATGCAGAAGTTGATGGGTATGGTGCAAGGACAAGAA 706
                                                                                                                                                                                                                                                                (1-1200)
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                                                                                                                                           4.16e-47
520.50
70.82%
43.78%
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514 bp mRNA linear EST 04-JAN-2002 PICL_19_C04.bl_A002 Pathogen-infected compatible 1 (PIC1) Sorghum Pany3243.
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Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
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Cordonnier-Pratt, M.-M., Gingle, A., Fang, G.C., Dean, R., Wing, R., Sudman, M. and Pratt, L.H.
An EST database from Sorghum: plants infected with a compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
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                                                        3 PheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLysGlyLys 22
                                                                                                                                                                                                                                                                                                                                                                                    63 SerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLyslleValGlnAspGlu 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 GluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAlaLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 LeuThrGluAlaAspIleLysIleMetArgGluValArgLeuAlaLeuPheGluAla
                                                                                                                                                                                                                                                                                                                                 192 GAIGITAGCCTTCCIGTIGTAAGAAGAITCGTTCAAACIGTAAGTGAACAAGCIGTCGGT
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                                                                                                                                                                                                                                                                           43 AspValAsnPheLysValValLysGluPheIleLysThrValSerGluArgAlaLeuGly
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
US-09-943-108A-2 (1-455) x BQ996389 (1-677)
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Fax: 706 583 0210
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669 ATGGATGAA 677
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                                                                                                                                                                                                                                                                           BQ996389 677 bp mRNA linear EST 22-AUG-2002 QGG12L07.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone BQ96389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project Intric/Compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu/
Belongs to contig QG_CA_Contig5305, see http://cgpdb.ucdavis.edu/
for details.
                                                  362 CAAGAAGCIGCAGCIITIGGICACAACAIICAAICICGAAAIIGGAAITACIGGIGCCAIC 421
                                                                                                                                                           GlnLysProlleLysPheValGlyMetSerGluLysLeuAspGlyLeuGlu 284
                                                                                                                                                                                            482 NGAAAGCCAATCAAGCTCGTAGGAAGGGGTGAACGTATGGAGGCCTTGAA 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
11. 1.(530)-742-1742
Fax: 1-(530)-752-9659
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Conservative:
Mismatches:
Indels:
Gaps:
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/db_xref="taxon:4558"
/clone_lib="bracks:
/clone_lib="bracks"
/clone_lib="bathogen-infected compatible 1 (PIC1)"
/tlsue_rype="Leaves"
/dev_stage="4-weaves"
/dev_stage="4-weaves"
/dev_stage="4-weaves"
/dev_stage="4-weaves"
/dev_stage="1-4-weaves"
/none="weaver.old seedlings infected with
collectorichum graminicola"
/none="weaver.old FRW421, as orghum isolate of the anthracnose
pathogen Collectorichum graminicola. Inoculated plants
were kept in a 25 C dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/2 hr of 19fht/dark
cycle at 25 C with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTs are expected to derive
from the host plant, no effort was made to eliminate ESTs
deriving from the pathogen."
below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement. Seq primer: JEN REV High quality sequence stop: 454 POLIXA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 GlnGluLysAlaLysAspLeuGluLysLysMetArgGluSerSerPheThrLeuAspAsp 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 ArgileLeuGlyMetGlyAspValLeuSerLeuIleGluLysAlaGlnGlnAspValAsp 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 GlyArgLeuHisIleAspGluAlaLeuMetAsnGluLeuLysGluValLysGluIleAla 213
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Mismatches:
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/cultivar="BTx623"
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QY 354 IleproGlyMetasnlysMet 360

CD 490 AFGCCAGGCATGAACAAGAFA 510
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Search completed: February 25, 2003, 03:09:37 Job time : 1571 secs

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-MODEL=frame+ p2n model -DEV=Xip
-MODEL=frame+ p2n model -DEV=Xip
-Q=/Cgn2_1/GSPTO_spool/US09943108/runat_21022003_151630_1801/app_query.fasta_1.647
-Q=/Cgn2_1/GSPTO_spool/US09943108/runat_21022003_151630_1801/app_query.fasta_1.647
-DE-GenEmb1 -OFMT-fastap -SUFFIX=sge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 - END=-1 - MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-OOTENT=P2TO -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09943108_GCGN_1_1_3745_erunat_2102003_151630_1801 -NCPU=6 -ICPU=3
-NO_ALREX -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGIAG -DEV_INMOUT=120
-WARN TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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4218.470 Million cell updates/sec
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                                                                                                                       February 25, 2003, 00:20:56; Search time 3139 Seconds
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                  2054640 seqs, 14551402878 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Sequence:
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30: em_htg_hum:*
31: em_htg_hum:*
32: em_htg_inv:*
33: em_htg_other:*
34: em_htg_pin:*
35: em_htg_pin:*
36: em_htg_ram:*
37: em_htg_vxt:*
38: em_sy:*
40: em_htg_ohum:*
41: em_htg_ocher:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	50 Signa	~ -	4826 Staphylo	16333 Sequence	591981 L	596170	113016 Sequence	117046 Sequenc	of Bacilius s	Z Bacilius	0707	0768	3191 Clostrid	4 Thermoan	5391	S 697	9	13 Seguence	9	ထွ		(3)	9	3 Segue	NOVEL IIR.	32 St	1153	400	2000	AE010044 FUSODACCE AF001802 Thermoton	3821	7276	339	280	150	8 Ei	491 ES	347 Escheri	2562 Es	004142 Vi	004793 Pseud	AE013692 Yersinia
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ALIGNMENTS

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C12M15/09, A61K31/00, A61K
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                                                                                                                                                                                                                                                                                                                Signal recognition particle polypeptide and polynucleotide Patent: JP 1999235183-A 1 31-AUG-1999; SMITHKLINE BEECHAM CORP
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JP 1992335183-A/1
31-AUG-1999
03-SEP-1998 JP 1998289963
03-SEP-1997 US 60/057890
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Strandedness: Single;
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Michael, T.B.
                                                                                                                                       JP 1999235183-A/1. unidentified.
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DB:
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440 320 340 540 200 220 240 260 300 900 ValLysAsnLeuGlyProLeuAspAspIleMetLysMetlleProGlyMetAsnLysMet 360 GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400 ArgIleAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420 360 420 160 480 180 009 999 720 780 GATGGTTTAGAGCTATTCCATCCTGAACGTATGGCATCACGTATTTTAGGTATGGGTGAT ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIle TyrSerGluGlyAspGlnValLySProGlnGlnIleValThrAsnAlaLeuLySHisAla LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla 421 AsnAspMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysLysGlyLys LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle 481 TACAGTGAAGGAGATCAAGTAAAGCCACAACAAATTGTAACTAATGCATTAAAACATGCT LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 541 AAAGAAGAACATTTAGACTTTGTAATCATTGATACAGCAGGTCGATTACACATCGATGAA ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln CTTGATGTCACAGGTGTTACCTTAACTAAATTAGATGGTGATACACGTGGTGGTGGTGACA TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu ArgAsnGlnMetGlnAsnMetLeuLysGlyMetAsnLeuProPhe 455

SOURCE

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BGAISSHERINGULSENELNAMDKALFTEIVYGTVKRKTTLDFILKPFVKTKIKÄWVRQ
LIMMST TYQYYLDKVPNHAININENEPETAKERGOGTHRONVWHYGLARPMSEDLEDFNEI
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GGEIIYSTCTIEQLENENVITTFLKNNKNFFFEDFFOHFITGELVKTLQIMPQDFNSDG
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LDATEERVSQIVINGIGEPFENYDEMMDFLRIVNDDNSLNIGARHITVSTSGIIPRIY
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LFGGVNDOLEHARELAHLIKGINCHVNLIPVNYVPVERNYVKTAKNDIFKFEKELKRLG
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PPPVKKVAMKYDLPVYQPEKLSGSEELEQLQLDVDLIVTAAFGQLLPESLLALPKLG
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QVFNQIRGLSPWPVAYTTMDDTNLKIYDAELVETNKINEPGTIIETTKKAIIVATNDN
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QIFEWLYQKRVDSIDEMTNLSKDLRQLLKDNFTVTTLTTVVKQESKDGTIKFLFELQD
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GEVASKFVTDELKSRFEAENLIEEHQAENWLRNNIKDINFQLYHYAQENAEYKGMGTT
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/translation="MSWEKENVSCOLFKWCAKHISHEETYMIENVKSLAFDIIODIIN
protein, similar to polypeptide deformylase"
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3155. ,4540
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/transl_table=11
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/gene="SA1061"
4543. .5637
/gene="SA1061"
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ELADYRFTKDSKGSSIKDVDAFFKGKKGIKRKVIETHDDVKQVDYMYVDPDGKKIGNS
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COMPLEMENT (1318. .1521)
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Aoki,K., Oguchi,A., Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K.
and Kikuchi,H.
                                                                                                                                                                                                        Staphylococcus aureus subsp. aureus N315 (sub_species:aureus N315,
                             AP003133 303750 bp DNA linear BCT 02-JUL.
Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-JAN-2001) Akio Oguchi, National Institute of rechnology and Evaluation, Botechnology Center; 2Chome 49-10 Nishihara, Shibuyara'ku, Tokyo 151-0066, Japan (E-mail:oguchi@hite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8427, Fax:81-3-3481-8424) On Jun 12, 2001 this sequence version replaced gi:13701012. Location/Qualifiers
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                                                                                                                                                                                                                                   strain:N315) DNA.
Staphylococcus aureus subsp. aureus N315
Bacteria: Firmicutes; Bacillales; Staphylococcus.
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21311952
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/gene="SA1057"
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/note="ORFID:SA1056"
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1820, .2308
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                                                                                                                                            AP003133.2 GI:14349175
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AP003133 BA000018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREKEETLKRFEREVHNSSOLSHONTVSMIDVDEEDCYYTVMEYIEGPTLSEYIESH
GPLSVDTAINFTNOILLDGIKHAHDMRIVHRDIKPONILIDSNKTLKIFDFGIAKALSE
TSLTQTNHVLGTVQYFSPEQAKGEATDECTDIYSIGIVLYEMLVGEPPFNGETAVSIA
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YQLNARVLVTKKDKTPIEKQFEINELLKIYENIGYETEFIGNDDDRRKIVEAMPAGLI
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8606. .9481
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/gene="cfxE"
9482. .10126
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/gene="cfxE"
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              Length:
Matches:
Conservative:
Mismatches:
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                                                                                       TTAGGTTCCGATGTAATGCAATCATTAACACCCAGGGCAAGTTATTAAAATAGTTCAA
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GluAlaAspValAsnPheLysValValLysGluPheIleLysThrValSerGluArgAla
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                                                                                                                                81 AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro
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/db_zer="dg1:14246765"

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                                                                                                                                                                                                                                RVGIARALALRPSLIVADEPVSALDVSVQSOVLNILKDIOBOFKLSYLFTAHDLSVVX
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ITMPQDRLKLKLKRQTRQLAAIYLASGIDPDKATLFIQSEVPAHVQAGWMLTTIASVGEL
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KSAYTDSDGIIKFDRDNKPGITNLISIYAGLTDMPIKDIEAKYEGGGYGKFKGDLAEI
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/gene="trpS"
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5177. .5572
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/transl_table=11
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/gene="oppB"
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Submitted (28-FBB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology: 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan
(E-mail:tohta@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lidan,J., Ito,T., Kanamori,M.,
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Mizutani-Oi,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamashita,A., Oshama,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
Whole genome sequencing of meticillin-resistant Staphylococcus
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TALNPVFTIKNQLVESIKSHKKISKKEANNLAKDLLKKVGIARQDEILNSYPHQLSGG
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VVAEFCDKVLVMYAGQIVEFGGIKEILHNPKHPYTQKLLSTIPKLKEGQKRLETIEGI
                                                                                                                                                                                                                                                                                                                                                                                                                   BCT 07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus subsp. aureus Mu50 (sub_species:aureus Mu50,
                                                                                                                                                         27566 AACGATATGAAGAAAATGATGAAACAATTCACTGGTGGCGGTAAAGGTAAAAGGTAAA 27625
                                    27506 CGTATTGCTAAAGGGTCTGGTCGTTCATTACAAGAAGTCAATCGTTTGATGAAAATTI 27565
                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete sequence, section 4/9.
AP003361 BA000017
AP003361.2 GI:14246761
401 ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
                                                                                                                 421 AsnAspMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysLysGlyLys 440
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On May 29, 2001 this sequence version replaced gi:13875305.
Location/Qualifiers
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300
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                                                                                                                                                                                                                                                                                                                                                                                           256910 TTAGGTTCCGATGTAATGCAATCATTAACACCAGGGCAACAACTATTAAAATAGTTCAA
                                                                                                                                              256730 AIGGCAITIGAAGGCTAATCAGAACGCCIGCAACGACGACGAAGAAAAAGCGTGGTAAG
                                                                                                                                                                                                                                                                                                               256850 GAGGCTGACGTAAACTTTAAAGTGGTAAAAGAATTTATTAAAACAGTATCAGAACGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256970 GAIGAAFTAACGAAGTIGGGIGGAGAAAAATACAITGATTAATAIGICAAATAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLys
                                                                                                                                                                                                                                               256790 GGTAAACTTACTGAAGCTGATATAAAGATAATGATGCGTGAAGTAAGATTAGCGTTATTT
                                                                                                                                                                                                                                                                                        GlualaaspValasnPheLysValValLysGluPheIleLysThrValSerGluArgAla
                                                                                                                                                                                                                                                                                                                                                                          61 LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 TyrargProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal
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                                                                                                                        MetalaPheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLys
                                                                                                                                                                                                         GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe
000
  Mismatches:
                                                                                  US-09-943-108A-2 (1-455) x AP003361 (1-347235)
  Best Local Similarity: 100.00%
Query Match: 100.00%
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                                                                                                                                                                                                                                               MDEINEBEDFVVEGPLMIQVHAPEKGYEVTISKSKNEDMMNSDDDATDQFDEQVQEL
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NPITTEFEDLLYMVDGTYYYAVHFDSHVDQEVINDSYSQLLEFAYPTDRTEVXLNDYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTFNLEKKOIMMFQOIQYLGGHKYVAEKRNAKIIELFNEAPCDYHAVYKLSKFAINQY
IKYCRWQNSVLEPTLSAMYQLQLTDQEVYYNYGYIFPEQIYIENHPIEWQLQVDLMLK
NGKSKLVNDNLNYFKLKKFIVALESKTALIEKLINNYLNICSDRGNDVQILF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFRNYÎKAYGAHNNTLGATLAGEVKKNVFNARTHNYKTARÊKALSNNHIPENVYDNLV
KTVHKYLPLIHRYTELRKELLGLDDLKWYDLYTPLIKDIKFEMPYEEAKEWMLKALEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGEEYLNVVKEGLNNRWVDVYENKGKRSGGYSSGAHLTNPFILLNWSNTISDLYTLYH
EFGHSAHSYFSRKFQPSNSSDYTIFVAEVASTCNEALLSDYMDKHLDDEKRLLILNQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LERFRATLFROTMFABFEHKIHAIBBAGEPLTPTRANBBYAKLNKLYFGDSVETDEDI
SKEWSRIPHFYMNYYVYQYATGYSAAQSLSHOILTBGKPAVDRYINEFLKKGSSNYPI
EIIKNAGVDWTTPBPIBQACBVPEQKLNAFBKLMKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÄHKHLAEQKCFNNETIKHYKSKLILAQMIQQGCKVEIEPFLKEIKQIPDILINNKYV
IELQYSPIPYKQILQRTEGLKKMGYKVSWLLNDVDYCHNKVKFNHFHSLFINPITRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEQFKGHIGDSAETLYNALELEDTLGTKLEKVYVYAHLKODODTYNDKYTGMESRAHQ
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/gene="SAV0999"
6783. .7769
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100.00%
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/traislation="makilipmotpdesttvlemliaehdvlavytqpdepvgekrymt
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NKNFEFEBPQHPITGELVKTLQIMPQDENSDGFFIIKIKRKDN
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hypothetical protein, similar to polypeptide deformylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein, similar to RNA-binding Sun protein" /codon_start=1
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                                                                                                 complement(1417. ,1695)
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AP004826 BA000033
AP004826.1 GI:21204263
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EBEROPDIEKYEBIEBKKMGJRDAPSLDKLDPLATEKSFTNSKGJQGNKDYKELAGKY
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ELADYRFTKDSKGSSIKDVDAPFKGKKGIKRKVIETHDDVKQVDYWYUPDGKKIGNS
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                                                                                                                                                   Db 257750 GTGAAAAATCTAGGACCACTGGATGATAATTATGAAAATGATTCCAGGTATGAATAAAAG 257809
                                                                                                                                                                                                                                                                                                                                                                     D 257930 CGTATTGCTAAAGGGTCTGGTCGTTCATTACAAGAAGTCAATCGTTTGATGAAACAATTT 257989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 257990 AACGATATGAAGAAATGATGAAGAAATTCACTGGTGGCGGTAAAAGGTAAAAAGGTAAA 258049
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Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Cui,L.,
Yamamoto,K. and Hiramatsu,K.
                   341 ValLysAsnLeuGlyProLeuAspAspIleMetLysMetlleProGlyMetAsnLysMet 360
                                                                                                                          LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIle 380
                                                                                                                                                                                                                               381 GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400
                                                                                                                                                                                                                                                                                                                                         401 ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Staphylococcus aureus subsp. aureus MW2"
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Direct Submission
Submitted (06-MAR.2002) Akio Oguchi, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus subsp. aureus MW2 (strain:MW2) DNA. Staphylococcus aureus subsp. aureus MW2
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome and virulence determinants of high virulence
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/protein_id="BAB94961.1"
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Lancet 359 (9320), 1819-1827 (2002)
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/gene="MW1096"
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CVCALVFEKSIVIANVGDSRAYVINSRQIEQITSDHSFYNHILVLIGGITPEEBATHPQ
RNIITKWMGTDKRVSPOLFIKRLNFYDYLLINSDGLTDYVKDNEIKRLLVKEGTIEDH
GDQLMQLALDNHSKDNYTFILAAIEGDKV"
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NEDVYELDKMYTIAVPLKKEDLAKHISEHKSNOPKRETTQVPIVNCAPHQQCKPEG
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IFNKNNLKLGKISRSYSDKYPENBIIKTTPNTGERVERGDSVDVVISKGPEKVKMPNV
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YQLNARVLVTKKDKTPIEKQFEINELLKIYENIGYETEFIGNDDBRKIVEAWPAGLI
VLSGQSGVGKSTFLNHYRPELNLETNDISKSLNRGKHTTRHVELFERQNGYIADTPGF
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SIGLPILDAVRAGFTLPIDVHLWHENPEKYIEAFBHGADMTSIHVESTPHIHRALQM
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                                   LDATEERVSQIVIMGIGEPFENYDEMMDFLRIVNDDNSLNIGARHITVSTSGIIPRIY
DFADEDIQINFAVSLHAAKDEVRSRLMPINRAYNVEKLIEAIQYYQEKTNRRVTFEYG
LFGGVNDQLEHARELAHLIKGLNCHVNLIPVNHVPFERNYVKTAKNDIFKPEKELKRLG
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GPLSVDTAINFTNQILDGIKHAHDMRIVHRDIKPQNILIDSNKTLKIFDFGIAKALSE
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LGIKQVYVEDFEHKSFSKAKKALEEKGFKVESKEEYSDDIDEGDVISQSPKGKSVDEG
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                 GYTIETVLMRHDYGNSVCVTTQVGCRIGCTFCASTLGGLKRNLEAGEIVSQVLTVQKA
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hypothetical protein, similar to protein kinase"
/codon_start=1
/codon_start=11
/protein_id="BABS4968.1"
/db_xref="G1:21204271"
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/protein_id="BAB94969.1"
/db_xref="GI:21204272"
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/db_xref="GI:21204270"
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/483. RA77
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26463
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Matches:
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                                                                            GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe
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                                                                                                                                                                                                              GIGAAAAAICIAGGACCACIGGAIGAIATIAIGAAAAIGAITCCAGGIAIGAAIAAAAIG 27483
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471 c 420 q 832 +
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Conservative:
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Patent: WO 0228891-A 3324 11-APR-2002;
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Sequence 3324 from Patent W00228891.
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Listeria monocytogenes ATCC 19115
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Location/Qualifiers
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AX416333.1 GI:21448790
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1719.50
86.81%
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VGLHIFVDIFNAYGTRURGITHSLEWIAFGFINTFDWFIFGSHVVAIAAWLLGSPVLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVTLYVILALYYVARFVTGRMIKHAVQNLIPDSEBIIIASTIHFFGWRVAVTTKDHYY VGRAFKRNISIYRKFDRLPYPDNBIIRSAKKDKNLAAFISSKYVNWRIBEKLDGTYV TFTDLRYRSNGHYPFVAVVKLDDDLKIVSSYTGWIFSTEKLYKKIAPVSI" complement(join(3130. .3147,3156. .3617,3625. .3630)) //gene="lmo1691" 3130. .3147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKVRGFEVVNEASRKFPEQTISLPIRGDKGSAGYDFFSNETVTI
VPGEKHIFWTDIKSYMQEDEVLNIYVRSSIGIKKGLLLCNGTGIIDSSYYSNPGNDGN
IGIAIKNFSNEPVSIEAGERVAQGVFQKYLVADTDIVANESRVGGVGSTGR"
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/translation="MYTYLDELFABLMVKNPHLDKEQALWWIEMLWSDFESSYAKAGY
                                                                                                                                                                                                                                                                                   EAHKNGVETNYPVKIKKVKMKTKELLSIIVISEDGKIAIEKRPENGLLANMWQFPTIE
ISKKENDEVAKLQFIHNYGLEVLLEDEPIAHIKHVFSHLVWKMDIRVAKLQSAIPNEN
                             /note="similar to A/G-specific adenine glycosylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to deoxyuridine triphosphate
nucleotidohydrolases"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to hypothetical proteins"
                                                                                                                                                                                                                                                                                                                                WYFATEEEMKRLAFPVPYCKWWQAWKDFKGE"
complement(850. .855)
/gene="lmo1688"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(2129, .3123,3130, .3147)
/gene="lmo1690"
2129. .2134
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/db_xref="GI:16411145"
/db_xref="SPTREMBL:08Y6J3"
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/gene="lmo1690"
complement(3130. .3147)
/gene="lmo1691"
complement(3156. .3617)
/gene="lmo1691"
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/db_xref="GI:16411146"
                                                                               /transl_table=11
/protein_id="CAC99767.1"
/db_xref="G1:16411143"
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complement(3629, .3862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1948. .1953)
/gene="lmo1689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3625. .3630)
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/gene="lmo1688"
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/trans1_table=11
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/transl_table=11
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2143, .3123
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  /qene="lmo1689"
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Baquero, F., Berche, P., Bloecker, H., Brandt, P., Chakraborty, T.,
Charbit, A., Chetouani, F., Couve, E., de Daruvar, A., Dehoux, P.,
Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L.,
Dussurger, C., Ettian, K.D., Fshih, H., Portillo, F. G., Garrido, P.,
Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T., Hauf, J.,
Jackson, D., Jones, L.M., Raerst, U., Kreft, J., Khuh, M., Kunst, F.,
Kurapkat, G., Madueno, E., Maltournan, A., Vicente, J. M., Ng, E.,
Nedjari, H., Nordsiek, G., Novella, S., de Pablos, B., Perez-Diaz, J. C.,
Purcell, R., Remmel, B., Rose, M., Schlueter, T., Simoes, N.,
Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and Cossart, P.
Comparative genonics of Listeria species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNKVALVTGSSRGLGRETAIALAKEGYDIAVNFSRNRKKAEEVQ
QEIEQLGRKCVIFKANVGDVEKVRELFKAVDEEFGRLDIFINNAASGVLRPLMELEES
HWDWTMNINAKALLFAGQBAAKLMQRHQSGKIISLSSIGSIRYLENYTYGVSKAAVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          ALS91981 ALS91824 347050 bp DNA linear BCT 06-JUN-20 ALS91981 ALS91824
381 GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400
                                                                                                    ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
                                                                                                                                 421 AsnAspMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysLysGlyLys 440
                                                                                                                                                                                                                                      526 AAGTCAATGACCAAAAATGAAAAAGACAATCCAGATATCATCAATGCAAGTAGAAGAAA 467
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complement(join(845. .1942,1948. .1953))
/gene="lmo1689"
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Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87
                                                                                                                                                                                                                                                                                                           441 ArgAsnGlnMetGlnAsnMetLeuLysGlyMetAsnLeuProPhe 455
                                                                                                                                                                                                                                                                                                                                                             ------AATCCATTCGGCAATTTCAAAATGCCATTT 317
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1. .347050
/organism="Listeria monocytogenes"
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Glaser, P., Frangeul, L. and Rusniok, C.
Direct Submission
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/db_xref="GI:16411142"
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/db_xref="taxon:1639"
complement(95. .841)
/gene="lmo1688"
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/gene="lmo1688"
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Listeria monocytogenes
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PUBMED
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JOURNAL
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KEYWORDS
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Db 121936 GTCGCCGCGCGCTTATGAAAACCTAACACCCGCCAACAACTTATCAAATGCTTCAA 121877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla 260
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                                                                                                                                                                                                                                                                                                                                       GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe 40
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                                                                       Conservative:
                                                                                                Mismatches:
                        Length:
Matches:
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                      2.22e-93
1717.50
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72.75%
75.53%
                                                                                                   Best Local Similarity:
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                        Pred. No.:
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AXIITYVILGCAFTRTLAKYSEMQALFLGTVLLCLFLARNEFYREKTYT
SIIFIVCLAGYIVIGGLARNIARSKELVYTWGSVUIIN
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DKMVIMGEPTGNMDKMEAAIEEVMMNADRFGYRPVFYEVRGTMIPYLHDHGFDFIKLG
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GREEKGFSLGFFDTYYLEQAPIAIAKNGEGTIVGFASMMPSYTDEWTSIDLMRYSKEA
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KSKPKLWINASAIGATISSKSTIYLDTEENTYADNPLGKTVYEWEKTASAASDLGIRV
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INGVVNFTAPHPVQEKKFAERLGKKMHKPTKTPVPKKIIKFILGERAMTILDSQRAYP
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complement(3872. .3877)
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VIGINTTGHPVKPFSKTVAMTDLEKVAPLADFFVSVLPQTEETSGIYQLSFFEKMKTN
AVFINIGRGSAVBLETLERASKEEQIAHFYLDVLPEEPLPAESYLWQASNVTITPHVS
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ABGFLEANNELAHENGSIJVIYDEVITAFRFWGGAQNYLGVIPDLTAMGKIIGGGLPI
GAYGGRVDIMEKVARLGFAYGACTHAGNPASILSGIACLEVLQEEGLYDRFEKYGSML
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INLAESKYEAWFITSAHSEADLLETIQAVDTYFGKLVQGK"
join(11879. 12981,12990. 13016)
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/db_xref="G1:16414295"
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TYGSNITEEKIKKAITULKLINVFSAGVDSLPTKIIQEQKIKVANVRGIHAIPMGEYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MDHSMSKKLHDEALLHIVGGVNSPSRSNKGVGGGIPVTMERANG
AYFYDVDGNKYIDYLAAFGPIITGHAHPHITEAITKAAQNGVLYGTPTKHEITFAKML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IYRSLEGNFPNMSVATVYNNLRVFRDAGLIKELSYGDASSRFDFSTSNHYHAICNVCG
KIVDPRFPGGLDEYGHFAANTGYBIDNHRLEVYGTCPECKEKQSNN"
complement (3930. .9335)
/gene="lin1791"
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                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to transcription regulators (Fur family), PerR in B. subtilis"
                        86.53
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/protein_id="CAC97024.1"
                      /note="tRNAscan-SE vs 1.3 result - Cove score =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(9405. .10346)
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/note="similar to glycerate dehydrogenases"
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/gene="lin7792"
/dene="lin87797"
/gene="gsab"
10476, .10481
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/db_xref="GI:16414294"
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                                       complement(3503. .3612)
/gene="rRNA-5s"
                                                                                                                       complement(3693. .6623)
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                                                                                                                                                                    complement(3693. .6623)
/gene="rRNA-238"
                                                                                                                                                                                                                                                      complement(6869. .8423)
/gene="rRNA-16s"
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/gene="lin1791"
                                                                                    complement(3503. .3612)
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/gene="rRNA-16s"
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/product="tRNA-Val"
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11879. .11884
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/gene="gsaB"
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Db 138781 TIAGAAATTACCGGCGTIGTAITAACAAAATTAGACGGTGATACACGTGGTGGGGGCAGCA 138722
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                                                                          281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
                                                                                                                             ValLeuSerLeulleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu
                                                                                                                                                                               321 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Listeria innocua, genome and applications
Patent: WO 0228691-A 7 11-APR-2002;
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Mismatches:
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AX413016
AX413016.1 GI:21445474
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                                    D 188164 GAAGAATTAACAAGCCTCATGGGCGGCGAAGAAAGTAAAATCGGAACAGCTGATCGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla
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MetalaPheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLys
                                                                                                                         GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe
                                                                                                                                                                                                                                                  41 GluAlaAspValAsnPheLysValValLysGluPheIleLysThrValSerGluArgAla
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1. 349980

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Abore="lasteria innocua"

Abore="seq 2058; Original length: 3.011.208 replaced

Anote="seq 2058; Original length: 3.011.208 replaced

by-seq 2058: 0.000.001 to 0.349.980-seq 4032: 0.300.001 to

0.549.980-seq 4035: 0.500.001 to 0.949.980-seq 4034:

1.800.001 to 2.149.980-seq 4035: 1.200.001 to

2.449.980-seq 4035: 2.400.001 to 2.749.980-seq 4040:

2.700.001 to 3.049.980-seq 4041: 3.000.001 to 3.011.208"
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                                                      GlnSerWetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400
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  LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIle 380
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                                                                                                          ArgIleAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe
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Matches:
Conservative:
Mismatches:
Indels:
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Listeria innocua, genome and applications
Patent: WO 0228891-A 4037 11-APR-2002;
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AX417046
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128842 128722 128541 GAACAAAAAAGAGAAAAGACAAGCATGACCTTAGATGACTTCTTGGACCAATTGCAACAA 128482 128422 :::||| |||||||||||||| ||| :::||| TTTCTCTAGGGATCAAGTAAGCA 128962 128841 GTAGTTGATTCAATGACTGGGCAAGACGCAGTAAATGTGGGCCCAAAGCTTCAACGAACAA 128782 CCAACCGTTATTATGATGGTAGGTTTACAAGGAGCTGGTAAAACAACCACTTCAGGAAAA 129142 260 320 340 161 TyrserGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180 381 GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400 TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal 160 LeuSerlleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu 280 GAAGAATTAAACAAGCCTCATGGGCGGGGAAGAAAGTAAAATCGGAACAGCTGATCGCCCG 181 LysGluGluHisLeuAspPheValllelleAspThrAlaGlyArgLeuHisIleAspGlu 128961 AAAGAAGAATTTAGAFTATGTCATTATCGATACAGCTGGTCGTCTTCATATCGAAA 321 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIle 118361 AAATCCATGACCAAAAACGAAAAAGATAATCCGGACATCATCAATGCGAGCAGCAGGAAAA 128901 ACTCTGATGGACGAATTAAAACAAGTGAAAGAAATCGCTACGCCAACTGAAATTTACTT ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla 281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLys 201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu

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Bacillus subtilis (strain:168) DNA.
Bacillus subtilis (strain:168) DNA.
Bacillus subtilis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
(bases 1 to 2739)
Honda,K., Nakamura,K., Nishiguchi,M. and Yamane,K.
cloning and characterization of a Bacillus subtilis gene encoding a homolog of the 54-kilodalton subunit of mammalian signal recognition particle and Escherichia coli Ffh
93328695
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GEKLDDALEBFHPERMASRILGMPULTLILERAÇASVDEDREKKELEGKRTRNESFLDDF
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                                                                                                                                    D14356 2739 bp DNA linear BCT 03-FEB-1999 Bacillus subtilis orfl, ffh, rpsP genes for ORPI, Ffh and 30S ribosomal protein S16, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAFEGIADRLQQTISKIRGKGKVSEQDVKEMAREVRLALLEADV
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SLGDQVSPVEIARQAIEKAKEBHYDYVILDTAGRLHIDHELMDELTIVKEIANPEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-FEB-1993) Kunio Yamane, Inst. Biological Sciences, Tsukuba University; Tsukuba, Ibaraki 305, Japan (Tel:0298-53-6419, Fax:0298-53-6006)
DD 128241 GCTGAAATGAAAAAAAGGTGAAGCAAATGACTGGTGGAGGAAAGGTAAGGAAAGGTAAA 128182
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365. .697
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2157. .2429
/gene="rpsp"
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/gene="ffh"
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Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Sekowska, A., Seror, S. J., Serror, P., Shin, B.S., Soldo, B., Sorokin, A., Tacconi, E., Takahashi, H., Takemazu, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Toseto, V., Uchiyama, S., Vandenbol, M., Vannier, P., Vassarotti, A., Viari, A., Wambutt, R., Wedler, H., Weitzenegger, T., Wincers, P., Wilpat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yeshida, K., Yoshikawa, H.F., Zumstein, B., Yoshikawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
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TSMAGPYSAVAALLKOANASLSYDEMED LITSTABETLDESTFPDSBYNDGYTEGLIVNA
FDAYSAYTDGLIGFAEGOV SVEDDOEPPYY GHEKYTEAT BEGGSLETTLDAEDNYGYTE
KLSYKLDGGEWTETTAKRISGDHLKGTYQAEIPDIKGTKLSYKWHIHDFGGHVVSYD
YYDVYRYKESTTAGYKOJFFAPROGYNASGTNNWBWGVPSTSTGDHRAAGSBKYYGYNLT
GNY ANSANNALWPPIKAPPIKAPSGSLFLOFKSHNLLEDDFYGYVYLPBGSEKVYCKY
YNGKTSSWTDEEIDLSAYKGQNIQVMFNLQSDESIAKEGWYIDDVYLSDKSAGKTVKK
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HVTGTMVGSEPDGTNQIGVAPGAKWIAVKAFSEDGGTDADII.EAGEWVLAPKDAEGNP
HPEMAPDVVNNSWGGGGGLDEWYRDMVNAWRAADIFPEFSAGNTDLFIPGGPGSIANP
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SDQSTGQYTLKHKAGDYTLMABAYGYQSKTQKVSLKTDQTQANFTLEBMKKGTLKGT
VINKTTGEPVTGASVYVVEDAAVEPAMTNDKGEYMLBAYEGAYTIKVAAPGYYSDEFS
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VQFPEVEKVLPNEKRQLFKSSSPFNMKKAQKAIKATDGVEWNVDQIDAPKAWALGYDG
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SKGIMVDKDFYLVYIQSKPDFYSPGLAMDETGQNSGRNWQYIDGKWQPGDKADGNYMI
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IDVNFDKPVISGLIPGEDKNLKAGESVKIAFSSAEDLDATFTIRMPLTNARASVQNAT
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                                                                                                                                                                                                                                                                                                                    The complete genome sequence of the gram-positive bacterium Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
Direct Submission
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/db_xref="G1:2633903"
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/BC_number="3.4.21,-"
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/gene="bpr"
/454. .5683
/gene="spoilga"
/gene="spoilga"
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                                                                                                                                                                    1131 GTCAGAAACATGGGGCCGCTTGATGATGAGATTCTGCAAATGATGATGCTGGGTGCAGGTAAATG 1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1911 GGGATTGCAAAAGGAAGGGGGACATCCGTACAGGAAGTCAACCGTCTGCTTAAGCAGTTT 1970
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LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu 280
                                                                                                                                 281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300
                                                                                                                                                                                                                                                                      ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
                                                                                                                                                                                                                                                                                                                                                                                                        GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
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GTFGASAIEKMAKIIAGIGELERHWSIMKSYPGFKPGTNTINPAVIEGGRHAAFIADE
CRIWITVHFYDNETHDOYAAEIEDSYNRLSDSDIWILRENRPYFKWGSSMIEDRREIF
PALEYDPGHPGYLATASAPKKRECPIIDVSQSYTDGGWLYDAGIPCYIYGPGDLHN
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AGTLECCKRGYHADFAIVADTSDMHIQQGGGVITGWIEIKSSQTFHDGTRRNMIHAGG
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TITLE Reidentification of facultatively alkaliphilic Bacillus sp. C-125 to Bacillus halodurans  JOURNAL Biosci. Biotechnol. Biochem. 63, 943-945 (1999)  REPERBUCE 3 (sites)  AUTHORS Takkami.H., Nakasone,K., Ogasawara,N., Hirama,C., Nakamura,Y., Masui,N., Fuji,F., Takaki,Y., Inoue,A. and Horikoshi,K.  TITLE Sequencing of three lambda clones from the genome of alkaliphilic Bacillus sp. strain C-125  JOURNAL Extremophiles 3 (1), 29-34 (1999)  MEDLINE 99184646  MEDLINE 99184646  A (sites)  AUTHORS Takami,H., Takaki,Y., Nakasone,K., Hirama,C., Inoue,A. and Horikoshi,K.  TITLE Sequence analysis of a 32-kb region including the major ribosommal protein gene clusters from alkaliphilic Bacillus sp. strain C-125  JOURNAL Biosci. Biotechnol. Biothem. 63 (2), 452-455 (1999)			PUBLEED 10972189  REFERENCE 10 (sites)  AUTHORS Takami, H., Nakasone, K., Takaki, Y., Maeno, G., Sasaki, R., Masui, N.,  FULI, F., Hirama, C., Nakamura, Y., Ogasawara, N., Kuhara, S. and Horikoshi, K.  TITLE Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28 (21), 4317-4331 (2000)  MEDLINE 20512582  PUBMED 11058132  REFERENCE 11 (bases 1 to 303249)  AUTHORS Takami, H. and Takaki, Y.  TITLE Direct Submission JOURNAL Submitted (22-Mar.2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group; 2-15 Natsushima, Yokosuka, Kanagawa 237-0061, Japan (E-mail:takamih@jamstec.90:p), URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html, Tel:81-468-67-3895, Rax:81-468-66-6364)  COMMENT On Jan 31, 2001 this sequence version replaced gi:10174886.
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                                                                                                                                                                                                                                                                                                                   'product="heat shock protein class I (low molecular
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Matches:
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Best Local Similarity:
Query Match:
DB:
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FEATURES
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SOURCE Bacillus licheniformis.  ORGANISM Bacillus licheniformis  Bacteria; Firmicutes; Bacillales; Bacillus.  REFERENCE 1 AUTHORS Berka,R. and Clausen,I.G. TITLE Methods for monitoring multiple gene expression JOURNAL Patent: WO 0.202113-A 1047 11-APR.2002;  REATURES 1.Cocation/Qualifiers Source 1.1136 //Ob.xref="taxon:1402" //Ob.xref="taxon:1402"  ORIGIN 338 a 263 c 326 g 209 t	dd. No.: 4.68e-77 Length: 1136  ore: 1402.00 Matches: 270  recent Similarity: 87.30% Conservative: 60  st Local Similarity: 71.43% Mismatches: 48  ery Match: 61.65% Indels: 0  c.99-943-108A-2 (1-455) x AX433432 (1-1136)	Oy 1 MethlapheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLySwetArgGlyLys 20	Oy 61 LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGln 80 :::		Oy 161 TyrSerGluGlyAspGlnValLySProGlnGlnIleValThrAshAlaLeuLySHisAla 180	201 Alliliiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
210074 141 210014 161 209954 181 209894	Oy 201 AlaLeukestanGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220          :::        :::	261 LeuSerIlehrgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu 280	209534 GTGCTGACACTCATFGAAAAAGCACAATCCACTGTCGATGAAGAAAAAGCAGGAACTT 321 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGluclareagGln 109474 GAGAAAAAATGCGTACAATGGATTAACGTTCGATGATTCTTGGAGCAATTCTGCACCAACAACAAAATGCACAAAAATGCAAAAAAAA	OY 301 LEVELYLEDASPLYSLEDASPORTS CANDERS CANDERS LEGISTATED BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT BY STATEMENT STAT	421 AsnAspWetLysLysMetMetLysGlnPherhrGlyGlyGlyLysGlyLysGly 439 209174 GAAGAAGARGAAAAGAAAGCAAATGAACAAAGCAAGAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAG	RESULT 13 AX433432 LOCUS DEFINITION Sequence 1847 from Patent W00229113. ACCESSION AX433432 VERSION AX433432.1 GI:21658236 KEYWORDS .

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FDNLKECESNTVDIYLNPKDISKLYSNKKTFFYSMKDKLNNLRINVIQNPEVEKDTLK
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Finishing, and Bioinformatics teams, Genome Therapeutics Corp., 100
Beaver Street, Waltham, MA 02453-8443, USA
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J. Bacteriol. 183 (16), 4823-4838 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium acetobutylicum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet 360
                              241 LeuaspValThrGlyValThrLeuThrLysLeuaspGlyAspThrArgGlyGlyAlaala 260
                                                                                                          LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu 280
                                                                                                                                                                                                                 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
                                                                                                                                      1081 AAAGGCTTAAAAAAAGGGGAAGGTTGAGTAAAAACAGCTCAGCCATATCGAAGCG 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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AE007684 AE001437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeualaLeuLeuMetArgLysLysTyrAsnLysProMetLeuValalaalaAspIle 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8187 TITICIATGGGGGATAAGGTTAATCCTGTTGATATTTCAAAGGCTGCAATGAAGCATGCT
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Mismatches:
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Matches:
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Query Match:
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VINAVGLQGAGKTIMCGKLSLSLKKKNKKPLLVACDIYRPAAIKQLEVVGKSIDVPVF
SMGDKVNPVDISKAAMKHAKENGLNVVIIDTAGRLHIDDQIANELENIKSEVNPKEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVVDSMTGQDAVNVAESFDNKLELTGVVLTKLDGDTRGGÅALSTREMTGKPTKVVGLG
EKMNDI EITPPDRAASTLGMCOVITTLLEKAGSATDENGASKEGLGNRAGSDENDDFL
QAPBOMKKLGPI GKRLLENVPGRNSSMLKGVDLSKNEGBAKKY EAL IT KSYPAKERKNPS
LITSTASRKRRIALGSGTTVQEVNKILKNFEDMKKMMKQFKGNKFSKRGLFGGKMPF*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Uncharacterized conserved protein, YLXM
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  QFIVITHRKGIMEASDVLYGVIMEEKGVSKVISLDLDSDRENVS"
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/transl_table=11
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/note="rpsP"
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/transl_table=11
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                                                           /note="ftsY"
6352. .7263
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complement(776. 1735)
/gene="blob"
//forte="319 aa, similar to pir:B70384 biotin synthetase (EC 2.8.16) from Aquifex aeolicus (332 aa); 43.4% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /traislation="MDFIERMEDKSLKNIKLTREBCLRLENSNLEELIKBANNIRKEI
HGDGIDLCSIINGKSGRCGEDCAFCAQSKYHKTNISEYPLLDYBKIKKVAKENEDEGY
HRFSIYYGSGLYGEPERYITYYSNINKELKILLCASHGIINKESLIKLKRAGYKRY
HHNLETSRNYDRICKCHRYEBERVETIKNAKRAGLEYCSGGIIGLEFTILDRIDLAIT
LRELEIKSIPINVLSAIKGTKLOMMIPLNEEEILRTIAVFRFINDEAKIRLAGGRYLL
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YKSVRDKYDFILCEGSGGIVCPISFSEKKLMLEDIIKEFNLOIILVSNSGLGTINYTV
LTVSYLRULGLKVKGIILNKFNKSDIIHRDNKKIIKELTGVNNISTVPKIEDIEKYDL
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NEKTURNLFLAQIIGLLYIYLEGYSYMYVIXNFYLGDAMSLLSAVSIQALACLPSD
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complement(2694. .3785)
                                                                                                                                  /note="228 aa, similar to sp:BIOD_METJA DETHIOBIOTIN
SYNTHETASE (EC 6.3.3.3) (DETHIOBIOTIN SYNTHASE) (DTB
SYNTHETASE) (DTBS) from Methanococcus jannaschii (248 aa);
33% identity in 221 aa overlap
CPE1543"
                                                                                                                                                                                                                                                                                                                                                                        /translation="MEKGVYIIGTNTDIGKTFISGLILKKLREEGRNAGYYKAVLSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="363 aa, similar to sp:YPUA_BACSU HYPOTHETICAL 31.3 KDA PROTEIN IN LYSA-PPIB INWERGENIC REGION (ORFX19) from Bacillus subtilis (290 aa); 31% identity in 271 aa overlap. Putative N-terminal signal sequence was found by SCOR?"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="184" as, similar to sp:BIOY_BACSH BIOY PROTEIN fr
Bacillus sphaericus (215 aa); 43.4% identity in 173 aa
overlap. Putative N terminal signal sequence and 4
putative transmembrane regions were found by PSORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNFGENAFKAGANATITGNLLTTCGNKIKDDKRLIENIGMRIF"
                        gas gangrene"
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/db_xref="GI:18145206"
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/protein_id="Bab81250.1"
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/gene="biox"
complement(1754. .2308)
/gene="biox"
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                                                                                        complement(87. .773)
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                                                                       /gene="bioD"
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CPE1544"
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13 DNA, complete genome, section 7/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (15-FEB-2001) Tohru Shimizu, Institute of Basic Medical
Sciences, University of Tukuba, Department of Microbiology; 1-1-1
Fennochda, Tsukuba, Ibaraki 305-8575, Japan
(E-mail:tshimizuemd.tsukuba.ac.jp, Tel:81-298-53-3354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium perfringens str. 13 (strain:13) DNA.
Clostridium perfringens str. 13
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                              9998
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8727 ATGABARAGTTAGGRCCTATAGGTAAGCTTCTTGRAATGGTTCCAGGTTTTAATAGTAGT .8786
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                                                                                                                                          378
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                                                                                                                                                                                                        ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
                                                                                                                                                                                                                                                                                                   321 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
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                 LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax:81-298-53-3354)
On Jan 14, 2002 this sequence version replaced gi:18145205.
Location/Qualifiers
1. 296750
                                                                                                                                                                                                                                                    341 ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLys---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---MetLysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleIleGlnSerMetThrProAlaGluArgAsnAsnProAsp-----ThrLeuAsnVal
                                                                                                            AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
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AP003191 BA000016
AP003191.2 GI:18146729
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Shimizu, T.
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AUTHORS
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gene

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/note="662 aa, similar to pir:S66017 formate dehydrogenase
homolog yyaE from Bacillus subtilis (667 aa); 32.1%
identity in 667 aa overlap
CPE1548"
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FLYEAEBIDEDIVNXIICNNKPPIFLYNKDKGEBLEIIDNEFLINKDKTLYRKALSEK
DKNKVIKKKLLKEINKVKELFDIDIIIGVDENPDVEEKSGVCTYIEDNFREKGSLSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITFEYLYALGMIKENIFKEVSKADFIGEGISNTARRTNEIIESALGGVLFIDEAYSLC
TDENDKAGREIVDALLKGIEDNRDNITVILAGYEKDMETFLSFNQGLKSRFPNVIKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYNPSEMYEIAVNIAKSKGYRIAKSAKAGLIELFTKNQMYGKSDLGNARFVRNIVENA
INDASKYLIVNKERALDLEKDNPHYKVSAKFDEBEKLERIGLEGVESFERSGYKLI
VAQREKKGYGVMYEIGONLOMIFAGRREGTGYTSIARLAVABKLINSGLLKYGCYJETDR
SSFVSDIPGETSKKTEBKFKEALGGYLFIDBAYTLANDSIGRBAIETLIKLIEDYSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYSELKKNFVELYENADAQSGNGRAVRNYVEQLIRNQSIRIAESDISVYEMNLINTKD
IKAMNAIKYDNHFDLEKKLNNLIGNEELKDFLRGQYKLAKIREKRKKLGFQVDLNKYM
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NIFLWGKNPANTTIHTWAILNKAKKNGSRIIVIDPINTQSAKLGDIHVKIKPGTDGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMAMAKIIISKGLQDKDFINKYVLGFQEYKDHLENFDLDYLSDECGIEIEDIEKLTKY
YCEKNSYSTITGYGMÇKYKNGKNIFABADALGATGGYGKGGGYWYANKYLSRIDSD
PPKSGEVGENREFYSKINEFIEFPKKYSLGYDDSNAPIKINVIANQLPKINK
INNSIDKYEFKVCFDMFWTDTASKCDLFIPCTNTLESEDMYFSSWTNPTLIYNEKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYDDVAWENKKFYTPSGKFELASKRALKECGSLTPTYLSPRIKENCFRLLTNHSKDSL
SSQHYIDVDEKAKVYLNENMIRKFSLICGEKVKLKSRTGEITAICSLDNGVQDTVALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIVILAGYEEEMENFFDVNIGLRSRFPLWTKFEDYNPNELLEMAIKLVEAKGFKLSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNYRFPIWVDFGNYNERELYDIASSTLVKKGFTLDEEAETALENAIGDIQKRMGELAL
KNGLMIKQFLDSLVRVQSIRVCDEDFDINTINRIISEDILKSTEIFLKKNTTQNGSF"
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                                KEAAREEISLTNNLSNAKTKOGGTLGKDEAAVVVNDIKTDVIKDKTKPKNDEEIGKIVNN
VTNNYNILLTQGQQEQTIKFMSKINDLDYNYGAMKESLNQMNDKLQQILKDTGKQLEE
SGLLEKALNGIKNVLVDIKDFLVNMFSSASEKVKOGITYDENGNIYIKTGNNSDESKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MLQKNIFVERKDMVNKEIIENGFFKIEKKLNEEFIGQKTFNKEL
CDYFKEKIEEDSKGILLIVEERDIFKNSVLKYFFEELNYYKFVKNSKIDEIDLAAYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QYISYKICKPIINIIRKEAIEANSRLLIYVEDDEIFCKSNDEVYDLSKYSNPTLEEVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKLESIIGMKELKEFIDKIENNFKVQKIREKLGLKTTQISLNMIFAGNAGTGKTNAAR
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NNLTEVTGSMLANALLTSGVNNADVKADAPFKVTGTAALAGILKGFEDASGEELSLPK
                                                                                                                                                                                                                                                                                                                             genes for CDase, GGTase, MBP and 15 OREs, partial and complete cds from Bacillus sp (549 aa); 45% identity in 522 aa overlap.Also similar to prf:2516401X stage V corpulation protein K from Bacillus cereus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10033. [11127
/gene="prs"
/note="364 as, similar to pir:A71345 probable
/hosphoribosyl pyrophosphate synthetase (prs) from
Treponema pallidum (421 aa); 32.3% identity in 325 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/rarasi_table=1
/product="probable formate dehydrogenase"
/protein_id="BAB81254.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="stage V sporulation protein /
/protein_id="BaB81253.1"
/db_xref="GI:18145210"
                                                                                                                                                        EESIQDKPQTQSNDNNQNQENEQGQNQTK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(7634. .9622)
                                                                                                                                                                                                                                                                               complement(4141. .7578)
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                                                                                                                                                                                                     complement(4141, .7578)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                         /gene="spovk"
                                                                                                                                                                                                                                          /dene="spovk"
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10033. .1112
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RESNGEGKVKIPQSVRGRDIYILCDIGNYSCTYKMFGFENHKGPDEHFQDIKRTVSAI
RGKARRITYIMPLLYEGRQHRRKGRESLDCALALOBLEKLGVDBYLTFDYHDPRWQNA
IPLMSFENYPTYDIYKSLIHNBKDDELDKEKLLVISPDTGAMDRAIYYSSYLGVDVG
LFYKRRDHSRIYNGKNPIVKHEYMGRDVDGKDVIJVDDMIASGESYLDIAKELKGRNA
RNYYARTFESFEGLEKRNKFPNDGIIKSYYSTNLTYIPBELNAAPWFKAVDLSDFI
ARIINKLNYDKSVASYMDATNIIQRLLDEK"
                                                                           /protein_id="BAB81255.1"
/db_xref="G1:18145212"
/translation="MNEQNHGLGIIALESCTELGNAIDKLIQEKRNCEESFLIKTDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184686 CTTGCATTGCACTTAAGAAAGAAA---AACAAAAGCCATTACTTGTGGCTTGTGATATA 184630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 184569 TTCTCAATGGGAGATAAGGTTAAGGCTGTAGATATTGCCAAAAGCTGCAATAGAGCATGCA 184510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185046 ATGGCTTTTGATGGATTAGCGTCTAAATTACAAGACACGCTTAAAAAATTAAAGGGTAAA 184987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 184986 GGTAAGCTAACAGAAAAAGATATAAAAGAAGCCATGAGAGAAGTAAAGCTTGCGCTTTTA 184927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD 184629 TATAGACCTGCAGCTATAAAGCAATTACAGGTIGTAGGAAAACAAATAGATATACCAGTA 184570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrThrThRAlaGlyLys 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GlualaAspValAsnPheLysValValLysGluPheIleLysThrValSerGluArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184806 GACGAATTAACAACTCTTATGGGAGAGACTGAGAGTAAATTAAAATACTCAGACAATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrargproalaalaileAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AspGluLeuThrLysLeuMetGlyGluAsnThrSerIleAsnMetSerAsnLysPro
                 /transl_table=11
/product="probable phosphoribosyl pyrophosphate
                                                                                                                                                                                                                                                                                                                                                            /note="353 aa, no significant homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="hypothetical protein"
/protein_id="BAB81256.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                     complement(11177. .12238)
/gene="CPE1550"
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                                                                                                                                                                                                                                                                                                                    complement(11177. .12238)
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                                                                                                                                                                                                                                                                                                                                   /gene="CPE1550"
                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=l
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.39e-73
1382.00
78.88%
62.70%
60.77%
                                                              svnthetase
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
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Db 183852 TCAAGAAAGAGAATAGCTAAAGGTTCTGGTACAACAGTACAAGAAGTAAAAGTC 183793
Db 184509 AAAGACAATGGAAATAACGTTGTTATAATAGATACCGCTGGTAGACTTCATATAGATGAA 184450
                                                                                                                                                                                                            Db 184089 AGTGAAAAAATGTTAAATCAAGAATTTAACTTTGATGACTACTTATCAGCTATGGATCAA 184030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D 183969 GAACTTGAAGGCATTGAT---TTTTCTCAAGGAGAAAAACAAATGGCTACAGTTAAAAGCT 183913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 MetLysGlnPheAsnAspMetLysLysMetMetLysGlnPheThrGlyGlyGlyLys--- 435
                                                               DD 184449 GATTTAATGCAAGAGTTAAAAGATGTTAAAGAAGTTTCAAATTCCTAGTGAAATATTATTA
                                                                                                                                                                                      LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla
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                                       201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu
                                                                                                                                                                                                                                                                  261 LeuSerIleArgSerValThrGlnLysProlleLysPheValGlyMetSerGluLysLeu
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Search completed: February 25, 2003, 02:59:00 Job time : 4087 secs

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Ffh gene: signal recognition particle; SRP; antimicrobial agent; vaccine; immunological response; gene therapy; infection; otitis media; conjunctivitis; toxic shock syndrome; septic arthritis; ss.
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-MONDEL_frame+_pro.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09943108/runat_21022003_151629_1790/app_query.fasta_1.647
-Q=/cgn2_1/USPTO_spool/US09943108/runat_21022003_151629_1790/app_query.fasta_1.647
-LOPEXT=0 -UINIOS-2PWT=fastap -SUFFTX=rnng -WINNATCH=0.1 -LOOPCE=0
-LOOPEXT=0 -UNINTS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MONDE=LOCAL -OUTRY=pct -NORM=ext -HEARSIZE=500 -MINIENO -NAXLEN=200000000
-USER=COS9943108_eCGN_1_1_396_erunat_21022003_151629_1790 -NCPG=6 -ICQN=3
-NO XLPXY -NO AMAP -LARGEQUERY -NG SCORES=0 -NAIT -LONGICG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                          February 25, 2003, 00:19:11; Search time 296 Seconds (without alignments) 3461.687 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                    OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                 2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext 0
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Run on:

Haemophilus influe Salmonella typhi D N. meningitidis pa Neisseria meningit

Neisseria meningit fragment #

Genomic

Staphylococcus aur Buchnera sp. genom Borrelia burgdorfe Helicobacter pylor Ehrlichia sp. E74 Staphylococcus aur Staphylococcus aur

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Mycoplasma genital

Streptococcus pneu S. aureus ffh codi Streptococcus pneu DNA encoding Strep

Staphylococcus epi Enterococcus faeca Enterococcus faeca

Listeria innocua

Staphylococcus aur Staphylococcus aur Staphylococcus aur Listeria monocytog

S. aureus ffh codi

Description

Bacillus lichenifo 2CFE 28 coding seq Streptococcus pneu Streptococcus pneu CFE 28 coding sequ Streptococcus pneu

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                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the Staphylococcus aureus signal recognition

particle (SRP) fih component. Fih polynucleotides are useful for

dadaposing a disease related to expression of fih polypeptides by

calaposing a disease related to expression of fih polypeptides by

calaposing of the presence/amount of fih polypeptides by

cala sequence encoding fih. Fih polypeptides and antaqonists are useful

cat sequence encoding fih. Fih polypeptides and antaqonists are useful

cat sequence encoding fih polypeptide levels. Fih polypeptides are useful

con thibit (antagonist) fih polypeptide levels. Fih polypeptides and antagonists by

chinding and observing the affect of fih polypeptide activity, which are

concential anti-microbial agents. Fih polypeptides and antigenic fragments

concential anti-microbial agents. Fih polypeptides and antigenic fragments

concentral anti-microbial agents. Fih polypeptides and antigenic fragments

concentral anti-microbial agents. Fin polypeptides are useful as antagonists, and

concentral anti-microbial agents. Fin polypeptides are useful as antagonists, and

concentral anti-microbial agents. Diseases diagnosed, prevented and treated

including otitis media, conjunctivitis, toxic shock syndrome, wound

care useful for bathing wounds and implants prior to surgical
                                                                                                                                                                                                                              New Staphylococcus aureus Signal Recognition Particle (SRP) with protein (ffh) and RNA (ffs) components - the SRP gene and protein useful as diagnostic reagents and for prevention and treatment of Staphylococci infections which cause otitis media, septic arthritis
                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 28; 35pp; English.
                                     98EP-0306741
                                                                      97US-0927216
                                                                                                        (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                       toxic shock syndrome
                                                                                                                                                                            WPI; 1999-169238/15.
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                                                                      10-SEP-1997;
                                     24-AUG-1998;
                                                                                                                                         Wallis NG;
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120 AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100 40 80 9 MetalaPheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLys 1 ATGCCATTTGAAGGCTTATCAGAACGCCTGCAAGGCGACGATGCAAAAAATGCGTGCTAGAAG GlyLysLeuThrGluAlaAspIleLysIleMetArgGluValArgLeuAlaLeuPhe LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGln G; 373 T; 0 other; 1368 455 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: (1-1368)288 BP; 521 A; 186 C; US-09-943-108A-2 (1-455) x AAX27221 3.47e-197 2274.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Sequence 1368 Alignment Scores: Pred. No.: Query Match: DB: 21 121 61 181 81 Score: ά

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                                               LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle
                                                            TTAGCATTATTGATGCGTAAAAATACAACAAAAAACCTATGTTAGTTGCAGCAGATATT
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                                                                      GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe 40
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                               ATGCCATTTGAAGGGTTATCAGAACGCTTGCAAGCGACGATGCAAAAAATGCGTGGTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr GJ;
                                                                                                               Staphylococcus aureus DNA for cellular proliferation protein #1643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                              Trawick JD,
                                                                                                                                          Antisense; ds; prokaryotic cellular proliferation gene;
antibiotic; antibacterial; drug design.
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2000US-242578P.
2000US-253625P.
                           AAS55331 standard; DNA; 1368
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                                                                                  (first entry)
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                                                                                                                                                                                      Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAU37472
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Yamamoto RT,
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23-MAY-2000;
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                                                                                  13-FEB-2002
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                                                       AAS55331;
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          1261 AACGATATGAAGAAAATGATGAAACAGTTCACTGGTGGCGGTAAAGGTAAAAGGTAAA 1320
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 LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIle
                                          GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys
                                                                                     ArgIleAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe
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                                                                                                                                                                          ArgAsnGlnMetGlnAsnMetLeuLysGlyMetAsnLeuProPhe 455
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                                                                                                                                                                                                                                                                                                                                         antibiotic; antibacterial; drug design
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2000US-242578P.
2000US-253625P.
2000US-257931P.
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2000US-206848P.
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Xu HH;
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Yamamoto RT,
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22-DEC-2000;
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programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO in this patent did not form part of the printed specification.
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Matches:
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           Staphylococcus aureus DNA for cellular proliferation protein #705.
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22-DEC-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonsa seruginosa and Enterococcus facealis. The promoniae, Pseudomonsa seruginosa and Enterococcus facealis. The convention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to intended to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
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                                                                                         ectides for the identification and development comprise sequences of antisense nucleic acids
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Mismatches:
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                                                                                                                                                                                  Seq ID No 8030; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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98.24%
98.24%
WPI; 2001-611495/70.
P-PSDB; AAU36534.
                                                                                            polynucleotides
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Best Local Similarity:
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181 541 201 601 221 199 241 721 261 781 281 841 301 901 321 961 341

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as probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaPheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1426 GAAGAACTAACAAGCTTAATGGGCGGAGAAAAAAGCAAAATCGGAACAGGGACCGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLys
                                                                                                                                                                                                                                                                                                               equences from Listeria species, useful for detection, prevention of infection, also related polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2256 BP; 533 A; 471 C; 420 G; 832 T; 0 other;
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Matches:
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antibodies and modulators
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   Listeria monocytogenes
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Query Match:
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                                      WO200228891-A2.
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TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180
                                                                                                                                                                                                                        ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln 240
                                                                                                                                                                                                                                                                                                LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla 260
                                                                                                                                                                                                                                               GTTGTCGATTCAATGACGGGTCAAGATGCTGTCAATGTTGCAGAATCTTTTGACGATCAA
                                                                                            CITGATGICACAGGIGITACCITAACTAATTAGATGGIGATACACGTGGTGGTGCAGCT
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                   LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu
                                                                                                                                                 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu
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ABQ70511 standard; DNA; 2256
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                                                            TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180
                                                                                              LysGluGluHisLeuAspPheVaIIIeIleAspThrAlaGlyArgLeuHisIleAspGlu 200
                                                                                                                                                                                                                                                                       AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300
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                                                                                                                                                                            LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla 260
                                                                                                                                                                                                                                      LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu 280
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The present invention relates to nucleic acid sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as an ornaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.

Note: The sequence data for this patent did not form part directly from MIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators
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                                             Antibacterial; Listeria; food contamination; mutational analysis;
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Listeria innocua contig DNA sequence #7.
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1708.50
86.59%
72.31%
75.13%
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CENT NAT
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                                                                                                                Listeria innocua
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(CNRS ) CNRS
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P-PSDB; ABP39950
                                                                                                                     Staphylococcus
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                                                                          188464 AAAGAAGAACATTAAGATTATGTCATTATCGATACACTGGTCGTCTTCATATCGACGA 188523
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Db 188164 GAAGAATTAACAAGCCTCATGGGCGGCGAAGAAGTAAAATCGGAACAGCTGATCGCCCG 188223
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                   161 TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla
                                                                                                                                                               181 LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu
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                                                              LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle
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                                                                                                                                                                                                                                                                                                                                                                                                               281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
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                                                                                                        141 TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal
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epidermidis; open reading frame; ORF; bacterial infection;
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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                                                                                                                                                        Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1958.
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Matches:
Conservative:
Mismatches:
Indels:
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1534.00
97.29%
92.47%
67.46%
ABN92495 standard; DNA; 1014
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Best Local Similarity:
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, thee essential genes themselves and the encoded proteins. The prokaryotes used are beneather soli, Staphylococcus aureus, Salmonella typhi, Klebsiella premonorae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

So when the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly formatives.
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273
86
89
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                    26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-235625P.
22-DEC-2000; 2000US-25931P.
16-FRB-2001; 2001US-269308P.
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1418.50
77.54%
58.96%
62.38%
                                                          2000US-191078P.
2000US-206848P.
                              21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                            Ohlsen KL,
Xu HH;
                                                                                                                                                                                (ELIT-) ELITRA PHARM INC
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P-PSDB; AAU33449.
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Best Local Similarity:
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                         21-MAR-2000;
23-MAY-2000;
27-SEP-2001
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P-PSDB; AAU35268.
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Yamamoto RT,
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22-DEC-2000;
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Pred. No.:
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 AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100
                                             ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrThrAlaGlyLys 120
                                                             LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle 140
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                     241 GAAGAATTAACGAAAACGTTAGGTTCAGAAACGGTTGAACTGAATAAATCTCCAAAAATC
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the grames, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella promuoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The protein is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to chem antibodies capable of binding to the expressed proteins. The proteins can be used to Screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
1321 GATCAAATGCTAGGTGGCGCGTTAAAGGCAAGTTAGGTAAAATG---GCCATGAATCGT 1377
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Xu HH;
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Db 961 GCTCAAAAAGGAAAACAGTTTGACTTTAACGATTCATGAGCAATTGGATCAA 1020 Qy 341 ValLysasnLeuGlyProLeuAspaspileMetLysMetileProGlyMetAsnLysMet 360   1021 GTTATGGGACTGACCATTGAACATTAAAAATGATCCCTGGAATGAGAATGATGATGAAGACTTGAAGACTTATAAAAATGATCCCTGGAATGAGAAACATG 1080   361 LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleIlele 380	Db 1081 CCTGGTATTGAAAATGTCAAAGTCGATCCAAAGATGGCACGGAAACGGGCGATGGTC 1140  Qy 381 GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400	401	421 ABBASPACLYS-LYS-AFFECT-NS-118-118-118-118-118-118-118-118-118-11	432	MecLeurys    :::    ATGATGAAG	SUL X12	AAX129/4; 19-MAR-1999 (first entry)	DE Enterococcus raecalis genome contig SEQ 1D NO:3/. XX XW Enterococcus faecalis; contig; detection; Enterococcal infection; XW vaccine; attenuation; computer readable medium; ds.	AX OS Enterococcus faecalis. XX PN W09850555-A2.	XX XX XY 04-MAY-1998; 98WO-US08985.	AA AA 14-NOV-1997; 97US-0066009. PR 06-MAY-1997; 97US-0044031. PR 16-MAY-1997; 97US-0046655.	AX. PA (HUMA-) HUMAN GENOME SCI INC. XX. PI Barash SC, Dillon PJ, Kunsch CA;				CC AAX12938 to AAX13919 represent these nucleotide sequences which are CC primary nucleotide sequences, also known as contigs. The computer-based
ore: 1418.50 Matches: 273  rcent Similarity: 77.54% Conservative: 86  st Local Similarity: 58.96% Mismatches: 89  ery Match: 62.38% Indels: 15  23.38% Gaps: 2  -09-943-108A-2 (1-455) x AAS53127 (1-1434)	Oy 1 MethlaphedludlyLeuSerGluhrgieuGhalaThrMetGhiysWethrgGlyLys 20	41 GlualaaspValasnPheLysValValLysGluPheIleLysThrValSel 	Oy 61 LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValHeLysIleValGln 80	OY 81 ASPGIULEUThTLYSLEUMEtGlyGlyGluAsnThtSerIleAsnMetSerasnLysPro 100 :::	OY 101 ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrThrThrAlaGlyLys 120	OY 121 LeualaLeuLeumetargLysLysTyrasnLysLysPrometLeuValalaalaaspile 140	OY 141 TYTATGPTOALAALAILEASDGINTAEVAIGIPLYSGINIIEASDIIEPTOVAI 160	OY 161 TYTSerGluGlyAspGlnValLySProGlnGlnIleValThrAsnAlaLeuLySHisAla 180	OY 181 LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200	QY 201 AlaLeuMetasnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 220	OY 221 ValValaspSerWetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln: 240	Oy 241 LeuaspvalThrGlyValThrLeuThrLysLeuaspGlyAspThrargGlyGlyAlaaha 260	OY 261 LeuSerIleargSerValThrGlnLysProIleLysPheVaiGlyMetSerGluLysLeu 280	QY 281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 300	OY 301 ValleuSerLeuIleGluLysAlaClnGlnAspValAspGlnGluLysAlaLysAspLeu 320	321 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln

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GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400
                                                                                                                                                                                              GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
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                                                 ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu
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                                                                                                                                                                                                                                                                                                                                 CCTGGTATTGAAAATGTCAAAGTCCAAAAGATGTGGCACGGAAACGGGCGATGGTC
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                                                                                    281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus licheniformis genomic sequence tag (GST) #1847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnAspMetLysLysMetMetLysGlnPheThr------
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2001US-279526P.
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system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis, or polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
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                                                                                                                                                  Sequence 6729 BP; 2131 A; 1181 C; 1357 G; 2053 T; 7 other;
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273
86
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115
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Mismatches:
Indels:
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Matches:
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells. The method is useful for monitoring cylobal expression of several genes from a Bacillus cell. discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in mitoring gene copy number variation and stability. Monitoring changes in which Bacillus cells adapt to changes in culture conditions, convironmental stress or other physiological provocation. Extensive tollow-up characterisation is unnecessary, when one spot on an array considering the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s patent did not form part of the printed in electronic format directly from WIPO
                                                                                                                                                                              Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 1847; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification, but was obtained
Clausen IG;
                                                                                       WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                     sequenced tag array
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Sequence 1136 BP; 338 A; 263 C; 326 G; 209 T; 0 other; Length: Matches: 4.18e-118 1402.00 87.30% 71.43% Alignment Scores: Pred. No.:

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CTCGGACAAGACGTTATGAAAAGCCTGACGCCGGACAGCAGGTCATTAAAGTGGTAAAA 240
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Mismatches:
Indels:
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1080 260 840 300 900 320 720 TyrserGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180 ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln 240 CITGCCAACCTGCTTCGCAAAAAAACATAACCGCAATCCGCTGCTCGCTGGCAGCAGACATC 420 TACCGCCCGGCGGCGATCAAACAGCTGGAAACGCTCGGCAAGCAGCTCGATATGCCGGTA 480 AAAGAAGAICAICACGACIACGIICICAICGAIACGGCGGGGACGCCIICAIAIIGAIGAA 600 Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE; CEG; Conserved Essential Gene; bacterial infection; antisense therapy; antibiotic resistance; ds. TTETCAATCCGCGCCGTGACAACACGCCGATCAAATTCGCCGGAATGGGCGGAAAGCTT AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 841 GATGCGCTGGAGCCGTTTCATCCTGAACGGATGGCTTCGCGGATACTCGGAATGGGCGAT 301 ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 321 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet GAGCTGATGGATGAGCTTGAGCAGGTAAAAGAAACCGCTCAGCCGGAAGAAGTTTTCCTT LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu :::||| |||||||:::||| ||| ||| :::||| TITICACTGGGGGAGATGCCAAGCAGGCCATCGAAAAGGCG AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu TyrargProalaalalleasnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 1081 AAAGGCTTAAAAAACGTGAAGGTTGAGTAAAAACAGCTCAGCCATATCGAAGCG 1134 LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAla 378 BP. AAH90837 standard; DNA; 1605 29-DEC-2000; 2000WO-US35604 (first entry) Streptococcus pneumoniae 28 coding sequence. WO200149721-A2. 02-OCT-2001 12-JUL-2001. AAH90837; 341 361 2CFE 541 601 241 261 281 361 141 421 161 481 181 201 221 199 721 781 RESULT 12 AAH9083 음 a g 셤 ğ 셤 셤 셤 ŏ δž ð δ Q Dp δ g ŏ g ğ qq  $\delta \gamma$ Q δŽ

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The present invention relates to nucleic acids (AAH90701-AAH90918)
encoding polypeptides (AAM01002-AAM0114), which are essential for the
viability of a bacterial cell wall. The acronym CFE stands for "CGG For
Expression", where CGG stands for "Conserved Essential Gene". The nucleic
acids are useful for detecting the presence of proteins essential for the
viability of a bacterial cell wall in samples such as cells, tissues,
biological fluids, blood, serum, nose, ear or throat swabs with
complementary sequences. The nucleic acids are also useful for
detecting corresponding target nucleic acid molecules with
complementary sequences. The nucleic acids are also useful for
determining whether a genomic nucleotide sequence of interest is
essential for viability of a bacterial cell or whether it resides within
an operon, by integrating an exogeneous nucleotide sequence comprising a
portion of an open reading frame of the genomic sequence of interest
which confers a selectable phenotype to the cell, and determining cell
viability with a selection agent such as chloramphenicol. The nucleic
acids and proteins are also useful as vaccines and for treating bacterial
infections with gene therapy and antisense therapy. The nucleic acids
antibiotic resistant bacterial infections.
                                                                                                                                                                                                         Nucleic acids encoding conserved essential genes involved in bacterial replication which are potential targets for the treatment of antibiotic resistant bacterial infections -
                                                                                                Bruccoleri RE;
                                                                                                Davison DB,
                                                                                                Dougherty BA,
                                                                                                                                                                                                                                                                                                  Claim 30; Fig 49; 380pp; English.
                                                (BRIM ) BRISTOL-MYERS SQUIBB CO.
  99US-0174089
                                                                                             Pucci MJ,
                                                                                                                                                              WPI; 2001-496721/54.
                                                                                           , TJ,
JA;
30-DEC-1999;
                                                                                           Dougherty
                                                                                                                     Thanassi
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Seguence 1605 BP; 484 A; 317 C; 393 G; 411 T; 0 other; Alignment Scores

AAS55519;

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1081 CCAGCCCTTCAAAACATGAAGGTGGATGAACGCCAGATTGCTCGTAAACGTGCCATTGTG 1140
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                                                              TATCGTCCAGCTGCCATTGACCAGCTTAAGACCTTGGGACAACAATGATGATGTGCCTGTC
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                                          TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal
                                                                                                   TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla
                                                                                                                              TITGCACTIGGAACAGAAGTACCAGCIGIIGAGATIGIACGICAAGGITIGGAGCAAGCC
                                                                                                                                                           LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu
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Note: The sequence data for this patent did not form part of format directly from MIPO at
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                                        Streptococcus pneumoniae DNA for cellular proliferation protein #90
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                                                                              Antisense; ds; prokaryotic cellular proliferation gene;
antibiotic; antibacterial; drug design.
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Mismatches:
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Matches:
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  (first entry)
                                                                                                                                              Streptococcus pneumoniae
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Xu HH;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets in the inthiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide vasity of organisms. The present sequence encodes an avide vasity of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
1141 TCTTCGATGACACCTGAAGAGGTGAAAACCCAGATTTGTTAAATCCAAGCCGTCGCCGT 1200
                                                                                      CGTATTGCTGCTGGTTCTGGAAATACATTCGTCGAAGTCAATAAATTCATCAAGGACTTT 1260
                                                                                                                                                                               ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe 420
                                                                                                                                  AsnAspMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysGlyLys 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae DNA for cellular proliferation protein #361.
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                                                                                                                                                                                                                                                                   -----GATATGAATAAAATGAAGCAAATGGGGGATTAATCCAAATAACCTTCCT 1350
                                                                                                                                                                                                                              ---AsnLeuPro 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                         ArgAsnGlnMetGlnAsnMetLeuLysGlyMet-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Seq ID No 9427; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                            BP.
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2000US-207727P.
2000US-242578P.
2000US-253625P.
                                                                                                                                                                                                                                                                                                                                                            standard; DNA; 1395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-191078P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC
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Xu HH;
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26-MAY-2000; 2
23-OCT-2000; 2
27-NOV-2000; 2
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Yamamoto RT,
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LysGluGluHisLeuAspPheValllelleAspThrAlaGlyArgLeuHisIleAspGlu 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGCCATTTGAAAGTTTAACAGAACGTTTGCAGAACGTCTTTAAAAATCTACGTAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyLysLeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 GluAlaAspValAsnPheLysValValLysGluPheIleLysThrValSerGluArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GAGGCCGACGTTGCCTTGCCTGTTGAAGGACTTTATCAAGAAAGTTCGTGAGCGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GAGGAACTGACAGCCGTTTTAGGTTCTGATACGGCAGAAATTATCAAGTCACCTAAAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 CCAACCATCATCATGATGGTTGGTTTACAAGGGGCTGGTAAAACAACCTTTGCTGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln
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                                                                                                                                                                                                                                                                                                                                                                                           1 MetalaPheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLys
                                                                             Sequence 1395 BP; 415 A; 272 C; 333 G; 375 T; 0 other;
                                                                                                                                                           1395
252
91
102
14
                                                                                                                                                                                                         Conservative:
Mismatches:
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Matches:
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format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences.
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Tue Feb 25

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bacterial
antibiotic
                                                                                                GCTGAGAAGATGCGCGAAAACACCTTTGATTTTAATGATTTCATCGATCAATTAGATCAG 1020
                                                                                                                                                                                                                     1261 AACCAGGCTAAACAGCTCATGCAGGGTGTTATGTCTGGG---------1299
                                                                                                                                          341 ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet 360
                                                                                                                                                                                                 361 LysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHisIleLysAlaIleIle 380
                                                                                                                                                                                                                                                         GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLysLys 400
                                                                                                                                                                                                                                                                                                                                                                     421 AsnAspMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysLysGlyLys 440
841 ACGGACATIGAAACCTICCACCCAGACCGCATGICTAGCCGIAICCITGGIAIGGGGGAI 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFG; Conserved Essential Gene; bacterial infection; antisense therapy; antibiotic resistance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bruccoleri RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AsnLeuPro 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to nucleic acids (AAH90701-AAH90918)
                                                     ATGCTCACTTTGATTGAGAAAGCTTCTCAGGAATACGATGAACAAAAAGCCCTTGAAATG
                                                                                                                                                           1141 TCTTCGATGACACCTGAAGAACGTGAAAACCCAGATTTGTTAAATCCAAGCCGTCGCCGT
                                                                                                                                                                                                                                                                                                                ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe
                          ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu
                                                                                  321 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes involved in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davison DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding conserved essential greplication which are potential targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                             441 ArgAsnGlnMetGlnAsnMetLeuLysGlyMet--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resistant bacterial infections -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH90724 standard; DNA; 1572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CFE 28 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-496721/54.
P-PSDB; AAM01025.
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c encoding polypeptides (AAM01002-AAM01114), which are essential for the viability of a bacterial cell wall. The acronym CFE stands for "CDE For Expression", where CEG stands for "conserved Essential Gene". The nucleic acids are useful for detecting the presence of proteins essential for the property of a bacterial cell wall in samples such as cells, tissues, biological fluids, blood, serum, nose, ear or throat swabs with ligands, complementary sequences. The nucleic acids are also useful for detecting corresponding target nucleic acids molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nucleotide sequence of interest is compressed in to viability of a bacterial cell or whether it resides within an operon, by integrating an expension nucleotide sequence comprising a portion of an open reading frame of the genomic sequence of interest comprising 200-500 base pairs) into the genomic sequence of interest which confers a selectable phenotype to the cell, and determining cell viability with a selection agent such as chloramphenicol. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids antibiotic resistant bacterial infections. 

Sequence 1572 BP; 479 A; 298 C; 384 G; 411 T; 0 other;

Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: DB:	3.26e-109 1306.00 74.73 54.90% 57.43%	Length: Matches: Conservative: Mismatches: Indels:	1572 252 91 102 2
∿6-60-sn	3-108A-2 (1-455	US-09-943-108A-2 (1-455) x AAH90724 (1-1572)	1572)	
QY	1 MetalaPheGluG	detalaPheGluGlyLeuSerGluArgLeuGln	uGlnAlaThrMetGl	1 MetalaPheGluGlyLeuSerGluargLeuGlnalaThrMetGlnLysMetArgGlyLys 20
qq	1 ATGCCATTTGAAA	GITTAACAGAACGITT	GCAGACGICTITAA	ATGCCATTTGAAAGTTTAACAGAACGTTTGCAGAACGTCTTTAAAAATCTACGTAAAAA 60
QY 2	1 GlyLysLeuThrG	SlualaaspileLysil	eMetMetArgGluVa	21 GlyLysLeuThrGlualaaspIleLysIleMetMetArgGluValArgLeuAlaLeuPhe 40
Dp qa	61 GGAAAAATCTCTG	GAAAAATCTCTGAATCTGATGTCCAAGA	GGCAACCAAAGAAAT	
Qy 4	41 GluAlaAspValA	AsnPheLysValValLy	sGluPhelleLysTh	GlualaaspvalasnPheLysValvalLysGluPheIleLysThrValSerGluArgAla 60
Db 121		SCCTTGCCTGTTGTAAA	: : :	
ΟΣ 6	1 LeuGlySerAspV	rAspyalMetGlnSerLeuThrProGlyGlnGlnValIleLysIleVal	rProGlyGlnGlnVa	61 LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGln 80
Db 18	181 GTCGGGCATGAGG	STCATTGATACACTTAA	TCCTGCGCAACAGAT	GTCGGGCATGAGGTCATTGATACACTTAATCCTGCGCAACAGATTATTAAAATCGTTGAT 240
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300 81 AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100 :::|||||||||| :::::||| :::
241 GAGGAACTGACGCCGTTTTAGGTTCTGATACGCCAGAAATTATCAAGTCACCTAAGATT ProThrValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLys 101 g δŽ

360 LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIle 140 301 121 임 δă g

TTGGCCAACAAAACTCAAAAAAAAAAAAAAAAAATGCTCGTCCTTTTGATGATTGCGGCGGGTTATT

420

TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 481 161 QΥ g

900 LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 541 CAAACTAATCATAACGACTATGTCTTGATTGATACTGCGGGTCGTTTGCAGATTGATGAG 181 Qγ g

AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu 201 ğ

1 1 660	24	G 720	a 260	r 780	u 280	T 840	008 d	T 900	u 320	: G 960	n 340	d 1020	t 360	T 1080	e 380	G 1140	s 400	; T 1200	e 420	T 1260	s 440	- 1299	54	350
:::	heAspAspGl	TTAATGCTCA	lyGlyAlaAl	GTGGTGCTGC	erGluLysLe	GTGAAAAGAT	lyMetGlyAs	GTATGGGGGA	laLysAspLe	CCCTTGAAT	InLeuAspGl	AATTAGATCA	ſetAsnLysMe ∣¦	TGGCAAACAA	ysalaileil	Grecarie	SerArgLysLy	AGCCGTCGCCG	fetLysGlnPr	TCAAGGACTIT	$\mathtt{sGlyLysLysGlyLy}$		AspleuPro 4	ACCTTCCT 1
	ValvalaspsermetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln	TGCGCGTGAGI	LeuAspValThrGlyValThrLustreuAspGlyAspThrArgGlyGlyAlaAla	CGATACTCGTG	LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu	CACTGGTACAG	AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp	CCGTATCCTTC	pGlnGluLys		GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln	TTCATCGATC	ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsnLysMet	GATTCCAGGT	eAspHisIleI	CCAGCCCTTCAAAACATGAAGGTGGATGAACGCCAGATTGCTCGTAAACGTGCCCATTGTG	GlnSerMetThrProAlaGluArgAsnAsnProAspThrLeuAsnValSerArgLySLys	GTTAAATCCAA	ArgileAlaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuMetLysGlnPhe	CAATAAATTC	yGlyLysGlyI		snglnMetGlnAsnMetLeuLysGlyMetAsnLeuPro	TAATCCAAAT
 	AlaValAsnVa	GCAGCCAATGI	LysLeuAspG1	AAGATIGAIGC	ProlleLysPh	CCAATCAAGTI	ArgMetAlaSe	CGCATGTCTAG	GlnAspValAs	CAGGAATACGA	ThrLeuAspAs	GATTTTAATGA	IleMetLysMe	TIGCICAAGAI	GluLysGlnIl	GAACGCCAGAI	AsnProAspTh	AACCCAGATT	LeuGlnGluVa	TICGICGAAGI	AsnAspMetLysLysMetMetLysGlnPheThrGlyGlyLy	GTTATGTCTGG	GlyMet	CAAATGGGGAI
:::::    FTCGTGATGTG	rGlyGlnAsp	<b>ITGGTCAGGAA</b>	alThrLeuThr	rcarcctracc	alThrGlnLys	FTACTGGAAAA	neHisProGlu	CCACCCAGAC	luLysAlaGln	AGAAAGCIICI	luSerSerPhe	AAAACACCIII	roLeuAspAsp	CGATGGAAGAC	euAsnMetSer	rgaaggtggat	laGluArgAsn	AAGAGCGTGAA	erGlyArgSer	CIGGAAAIACA	etMetLysGln	rcargeaggg	snMetLeuLys	AAATGATGAAG
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Search completed: February 25, 2003, 01:52:44 Job time : 421 secs Sequence 1980, App Sequence 18, Appli Sequence 1, , Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 1, Appli

Sequence 496, App Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2341, Appli

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APPLICANT: Black, Michael T.
TITLE OF INVENTION: SIGNAL RECOGNITION PARTICLE POLYPEPTIDES
TITLE OF INVENTION: SIGNAL RECOGNITION PARTICLE POLYPEPTIDES
TITLE OF INVENTION: AND POLYNUCLEOTIDES
TITLE OF INVENTION: AND POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/035,382
CURRENT FILING DATE: 1998-03-05
BARLIER FILING DATE: 1997-09-03
NUMBER: OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
US-09-134-001C-1980

US-08-888-207A-180

US-09-007-476-1

US-09-007-444-1

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US-09-007-444-1

US-09-007-444-1

US-09-007-444-1

US-09-007-448-3

US-09-007-484-3

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US-09-103-840A-1

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US-09-11-507-38

US-09-21-507-38

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA CAPANISM: Staphylococcus aureus US-09-035-382-1
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-MODEL=frame+_por_model_-DEV=xlp
-Cegn_2_1/GSPTO_spool_/US09943108/runat_21022003_151631_1864/app_query.fasta_1.647
-D=1csued_-Patente_NA -QFNT=fastap -SUFFIX=rni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -NNITG=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi
-LISST=AS_DOCALIGN=200 -THE_SCORE=pet -THE_MAX=100 -THE_MIN=0 -ALIGN=15
-MODE=LCCAL -OUTPMT=pto -NORM=ext -HEAPSIZE=-500 -MINIEN=0 -NALEN=200000000
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-NO_XLEXT -NO_MARP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGIAG -DEV_TIMEOUT=120
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 46, Appl
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Sequence 238, App
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1722.690 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-06-047-6
US-08-317-401E-1
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Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
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141 TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal 160
                                               TyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180
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                                                            LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu
                                                                                                                                          201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu
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OPERATING SYSTEM: MSDOS version 6.2 SOFWARE: ASCII Text
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ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
STRY: Rockville
STATE: Maryland
COUNTRY: USA
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APPLICATION NUMBER: US/08/961,527
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NAME: BLOCKES, A. Anders
REGISTRATION NUMBER: 35,373
REFERRINGE/DOCKET NUMBER: PB340P1
FELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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US-08-961-527-46/C
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Matches:
Conservative:
Mismatches:
Indels:
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                  TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 7577 base pairs
                                                                                                                                                                                                             4.91e-138
1306.00
74.73%
54.90%
57.43%
(301) 309-8504
                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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2133 ATGCTCACTTTGATTGAGAAAGCTTCTCAGGAATACGATGAACAAAAAGCCCTTGAAATG 2074
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                                      281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
                                                                ACGGACATTGAAACCTTCCACCCAGACCGCATGTCTAGCCGTATCCTTGGTATGGGGGGAT
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TITLE OF INVENTION: SIGNAL RECGNITION PARTICLE POL.
TITLE OF INVENTION: AND POLYNUCLEOTIDES
TITLE OF INVENTION: AND POLYNUCLEOTIDES
FILE REFERENCE: GMSO035
CURRENT APPLICATION NUMBER: US/09/035,382
CURRENT FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: 60/057,890
EARLIER FILING DATE: 1997-09-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
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Patent No. 6284515
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1305.00
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57.39$
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Best Local Similarity:
Query Match:
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GAGGCTGACGTAAACTTTAAAGTGGTAAAAGAATTTATTAAAACAGTATCAGAACGCGCA
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                                                           GluAlaAspValAsnPheLysValValLysGluPheIleLysThrValSerGluArgAla
                                                                                                                                           LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGln
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
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FastSEQ for Windows Version 2.0
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CORRESPONDENCE ADDRESS:
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AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu
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; Sequence 1, Application US/09385287
; Patent No. 6350857
; GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL
NUMBER OF SEQUENCES: 2
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Matches:
Conservative:
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           APPLICATION NUMBER: US/08/923,772
                                                                                                                        REFERENCE/DOCKET NUMBER: GM10080
                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
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1297.00
74.51%
54.68%
57.04%
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SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
  CURRENT APPLICATION DATA:
                                                                                                                                                                TELEFAX: 215-994-2222
                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                        TOPOLOGY: linear
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Best Local Similarity:
                           FILING DATE:
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ADDRESSER: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia ZIP: 19103

COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
OPERALING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:

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201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Matches:
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Mismatches:
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APPLICATION NUMBER: US/09/385,287
                                                                                                                                                                                                                                                                                                                                                                                               Indels:
Gaps:
                                                                                                                            GM10080
                                                                                                                                                                                                                                                                    TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                    APPLICATION NUMBER: 08/923,772
                                                                             ATTORREY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
           FILING DATE: 30-Aug-1999
CLASSIFICATION: <Unknown>
                                                                                                                          REFERENCE/DOCKET NUMBER: (TELECOMMUNICATION INFORMATION: TELEPHONE: 215-994-2252 TELEFRAX: 215-994-2222
                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                   FILING DATE: <Unknown>
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1297.00
74.51%
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                                       APPLICATION DATA:
                                                                                                                                                                                 TELEX: <Unknown>
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Best Local Similarity:
Query Match:
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Pred. No.:
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601 CTCCTCATGAATGAGCTTCGTGAATGTGAAAGTATTGGCTCAACCAAAATGTAGTGCTT
                                                                                                  841 ACAGATATCGAAACCTTCCACCAGACCGTATGTCTAGCCGTATCCTTGGCATGGGGGAT
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                                                                                                                                                                        LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla
                                                                                                                                                                                                     LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu
                                                                                                                                                                                                                                                                                                     281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
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Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
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GlyGlyAlaAlaLeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMet 276
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   137 AlaAlaAspIleTyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIle 156
                    157 AspileProValTyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAla 176
                                                                                            GGGGTACCCGTCTACAGCGACCGGACAGCAAAAAGCCGGTCGAGATAGCCCGACAGGC 622
                                                                                                                                          LeuLysHisAlaLysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeu 196
                                                                                                                                                                                                                                                                                   GluIleMetLeuValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSer 236
                                                                                                                                                                                                                                                                                                                                                      237 PheAspAspGlnLeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArg 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerGluLysLeuAspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeu 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 GlnLeuAspGlnValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGly 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 CAGATACATCAGATCAAAAAGATGGGTAACCTCAAAGAGCTTGCATCCATGATCCCGGGA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GTGGGA------AAGGCCATCAAGGATATCGACATAGACGACGACGATGCCTTCAAGAGCATC 28
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COUGHLIN, Richard T.
TITLE OF INVENTION WILE OF GRANULOCYTIC ERHLICHIA
USE OF GRANULOCYTIC ERHLICHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377 LysAlallelleGlnSerMetThrPro 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MURPHY, Cheryl STOREY, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        858 AAAGGCAGT---CCGGCAGTAATCCTGATGTCCGGATTGCAAGGTTCGGGTAAGACCACC 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 ThralaGlyLysLeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuVal 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              978 AAGGAAAAAGCCATCGGCCAAAACGIGCIGACCICCGICCGICCGGGCGAACIGAIGGIG 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 MetArgGlyLysGlyLysLeuThrGluAlaAspIleLysIleMetArgGluValArg 36
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                     27340-20021.00
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Gaps:
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ORGANISM: PORYPHYROMONAS GINGIVALIS
US/09/221,017B
                                                                                                                                                                                                                               PCT/AU98/01023
                                                         PP1182
PRIOR DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP154
FILING DATE:
                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 928:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 base pairs
                                                                                                                                                                                                                                                                                                    32,430
                                                                                                                                       FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
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1003.50
73.17%
51.49%
44.13%
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                  23-DEC-1998
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                 NAME: Monroy, Gladys H
REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
APPLICATION NUMBER:
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                  FILING DATE: 2:
CLASSIFICATION:
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TELEX: 7
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COMPUTER READABLE FORM:
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: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100
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          OPERATING SYSTEM: PC_DOS/MS-DOS
SOGTWARR: PATENTEN Release #1.0, Version #1.30
CURRAY APPLICATION DATA:
APPLICATION NUMBER: US/09/066,047A
FILING DATE: 24-Apr-1998
CIASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
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174
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147
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Matches:
Conservative:
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                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 106.941.156 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
Indels:
                                                                                                           APPLICATION NUMBER: US 60/044,869
FILING DATE: 25-8PR-1997
ATTORNBY/AGRNT INFORMATION:
NAME: Superko, Colleen
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 6:
COMPUTER: IBM PC compatible
                                                                                                                                                                     REGISTRATION NUMBER: 39,850
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO. 6: SEQUENCE CHARACTERISTICS: LENGTH: 4804 base pairs
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                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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853.00
63.57%
40.37%
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Best Local Similarity:
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DB:
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CORRESPONDENCE ADDRESS: ADDRESSEE: No. 59225610 No. 5922561disk of No. 5922561th America, Inc. 4147 GITGIAGACICCTTAAIGGGGCAAGAIGCCGTCACTAIGGIGCGCAAGIICAAIGAGGAG 4206 ||| |||||||:::|||||||||| ::: ||| :::::: GTCGCATCTTTGTAGAAAAGGCGGTAGAAGCGGTTGGCAAGGATACAATTAATGAGCTA 4446 4447 CAGGCGAAGGCCAAGAAGGGTAAATTCGATTTGGATGATCTTGTTATTCAGCTGAAAGCT 4506 |||:::|||| ||4567 ATAAAACGCAAAGTTGCGGGGATA------GCTGATGACAGCAAGTCGACATG 4614 GACATGATAGATGAGCTGAAGTGTGTAAAGAAGGAGGTATCACCAGCTGAAATTGTATTG 4145 300 396 ValSerArgLysLysArgIleAlaLysGlySerGlyArgSerLeuGlnGluValAsnArg 415 LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla 260 LeuSerIleArgSerValThrGlnLysProlleLysPheValGlyMetSerGluLysLeu 280 ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320 GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340 181 LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln 281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp 376 IleLysalaIleIleGlnSerMetThrProalaGluArgAsnAsnProAspThrLeuAsn 4615 TACATTGCGATTATTAACTCAATGACGAAGCAGGAGGGGCGAATCCTGAGATACTGAAT 201 AlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeu ValLysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMet----------AsnLysMetLysGlyLeuAspLysLeuAsnMetSerGluLysGlnIleAspHis Sequence 3, Application US/08317401E
Patent No. 5925561
GENERAL INFORMATION:
APPLICANT: Thompson, Sheryl Ann
APPLICANT: Taver, Debbie Sue
TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE
TITLE OF INVENTION: ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 10 4735 TTGCTAAAGCAGTATAATCAGATGAATTCGATA 4767 405 Lexington Avenue, Suite 6400 416 LeuMetLysGlnPheAsnAspMetLysLysMet 426 MEDIUM TYPE: Floppy disk σ

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81 AspGluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysPro 100
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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156
75
211
19
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Conservative:
Mismatches:
Indels:
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                                                                                                                              NAME: Harrington, James J.
REGISCRARION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4248.000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEPAS: 212 867 0288
INFORMATION FOR SEQ ID NO: 3:
                                                                       APPLICATION NUMBER: US/08/317,401E
FILING DATE: 03-October-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Aspergillus niger
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592.50
50.11%
33.84%
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LENGTH: 2166 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
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MOLECULE TYPE: c
ORIGINAL SOURCE:
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ADDRESSEE: No. 59225610 No. 5922561disk of No. 5922561th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
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198 ileAspGluAlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGlu 217
                                   674 CAGGAAGAAGCTTTTCACCGAAATGACCCAGATTCAGACCGCCGTCACCCCGGACCAG 733
                                                                                                                    734 ACCAICCICGICCICGACAGCACCATCGGICAGGCIGCCGAAGCCCAGTCCICGCCITC 793
                                                                                                                                                            AspAspGlnLeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGly 257
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APPLICANT: Thompson, Sheryl Ann
APPLICANT: Yaver, Debbie Sue
TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE
TITLE OF INVENTION: ASPERGILLUS NIGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08317401E Patent No. 5922561
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STATE: New York
COUNTRY: U.S.A.
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                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,401E
FILING DATE: 03-0ctober-1994
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
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193
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 4248.000-US
TELECOMONICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                                CDS
join (126..203, 253..1776)
                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      NAME: Harrington, James J. REGISTRATION NUMBER: 38,711
                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Aspergillus niger
                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISCIS: TRUTH: 2877 Dass pairs
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51.16%
34.65%
25.22%
                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                         linear
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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Sequence 20, Application US/08981527A
Patent No. 6410262
GENERAL INFORMATION:
APPLICANT: Ouax, Wilhelmus J.
APPLICANT: Kerkman, Richard
APPLICANT: Rockhuizen, Cornelis P.
TITLE OF INVENTION: No. 6410262el Secretion Factors for
TITLE OF INVENTION: Oram-Positive Microorganisms Genes Encoding Them and Method.
TITLE OF INVENTION: of Using It
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GlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeuAspValThrGlyValThr 247
                                                                                                                                                                                                                                                                                                                                       856 CAGGCTGCCGAAGCCCAGTCCTCCGCCTTCAAGGCCACGCAGACTTCGGAGCCATCATC 915
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CURRENT APPLICATION NUMBER: US/08/981,527A
CURRENT FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: PCT/NL96/00278
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                2471 GAAGAGGIICITATCAGCGGGATGICGGIITITACAACCGITAIGGAATTAATAGAIGAG 2530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluAsnThrSer---IleAsnMetSerAsnLysProProThrValValWetMetValGly 108
                                                                                                                                                                                                                                   4 GluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLysGlyLysLeu 23
                                                                                                                                                                                                                                                                                            24 ThrGluAlaAspIleLysIleMetArgGluValArgLeuAlaLeuPheGlu----- 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyGlnGlnValIleLysIleValGlnAspGluLeuThrLysLeu-----MetGlyGly 89
                                                                                                                                                                                                                                                                                                                                                     ----AlaAspValAsnPheLysValValLysGluPheIle----- 53
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                                                                                                    4370
114
66
120
38
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                                                                                                                                 Conservative:
                                                                                                                                                Mismatches:
Indels:
                                                                                                       Length:
Matches:
                                                                                                  6.96e-39
432.00
53.25%
33.73%
19.00%
                           TYPE: DNA ORGANISM: Bacillus subtilis
                                                                                                                                                Best Local Similarity:
                                                                                                                                  Percent Similarity:
                                                                                      Alignment Scores:
                                                         US-08-981-527A-20
ID NO 20
ENGTH: 4370
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                                                                                                    Pred. No.:
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Sequence 7, Application US/08981527A
Patent No. 6410262
GRNERAL INFORMATION:
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Guax, Wilhelmus J.
APPLICANT: Broekhuizen, Cornelis P.
TITLE OF INVENTION: Gram-Positive Microorganisms Genes Encoding Them and Methot TITLE OF INVENTION: Gram-Positive Microorganisms Genes Encoding Them and Methot TITLE OF INVENTION: Gram-Positive Microorganisms Genes Encoding Them and Methot GURRENT APPLICATION UNDMER: US/08/981,527A
CURRENT FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: PCT/NL96/00278
WINDER OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE
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84 GAAGAGGITCITAICAGGGGGAIGICGGTITTACAACCGIIATGGAAITAAFAGAIGAG 243
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                                                                                                                                 LeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAspValLeu
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                                                                                                                                                                                    24 ThrGluAlaAspIleLysIleMetAngGluValArgLeuAlaLeuPheGlu-----
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                                                                                                                                                                                                                                                                                                             SerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu 320
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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Best Local Similarity:
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US-08-981-527A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 SerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAlaLys 181
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                                                                                                                                                           358 TTCTTCGAAGCTCTGGAAGAATG------CTTATTACTGCGGACGTGGTTTTAAT 408
                                                                                                                                                                                                                                09 ACCGITATGAAATTAACTGATGAGCTACGIACAGAAGCACAAAGACGIAATAIACAAGAA 468
                                                                                                                                                                                                                                                                                                                                        GluLeuThrLysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysProPro 101
                                                                                        298 CAAAACTTCCAAGAACAGTTAAATAATTAATTGCTCGATATAGAAAAGTTGACGAAGAT 357
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1045 aaagggggtattgtattagcaattggaaatgagttacacattccagttaaatgtggt
                                                      GluargLeuGlnalaThrMetGlnLysMetArgGlyLysGlyLysLeuThrGluAlaasp
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                  JS-09-943-108A-2 (1-455) x US-09-134-001C-1980 (1-1248)
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FITLE OF INVENTION: DEPENDANCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR RILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
SEQ ID NO 1980
LENGTH: 1248
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                                                                                         ProGlnGlnIleValThrAsnAlaLeuLysHisAlaLysGluGluHisLeuAspPheVal 188
                                                                                                                                                                                                                                              CCGCCGCCTGTCATCTTCATGCTGTTCATGCTGCGAAAGCAAGAAATGCCGATGTATTA 636
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LeuGlnGlyAlaGlyLysThrThrAlaGlyLysLeuAlaLeuLeuMetArgLysLys 128
                                                                                                                                          LeuGlnThrValGlyLysGlnIleAspIleProValTyrSerGluGlyAspGlnValLys 168
                                                                                                                                                                            CTGGAAGTATGGGGAGAGCGTACAGGAGTGCCTGTCATTAAGCAGGACGGCAGGAAGCGAT
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Matches:
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US-09-134-001C-1980
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       633 GAGGAACTGACAGCCGTTTTAGGTTCTGATACGGCAGAAATTATCAAGTCACCTAAGATT 692
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
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Matches:
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Patent No. 6159949
GENERAL INFORMATION:
APPLICANT: Black, Michael T.
TITLE OF INFENTION: No. 6159949el FtsY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/007,476 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GM10079
                                                                                                                                                                                                 141 TyrArgProAlaAlaIleAsnGln 148
                                                                                                                                                                                                                                     813 TATCGTCCACCTGCCATTGACCAG 836
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TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1251 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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55.59%
31.37%
18.51%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Falk, Stephen T
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COM
OPERATING SYSTEM:
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COUNTRY: U
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US-09-007-476-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 GluAlaAspValAsnPheLysValValLysGluPheIleLysThrValSerGluArgAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGln 80
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Indels:
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FastSEQ for Windows Version 2.0
                                                             APPLICANT: Black, Michael
APPLICANT: Hedgson, John
APPLICANT: Knowles, David
APPLICANT: Stocholas, Richard
APPLICANT: Stochola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
WUMBER OF SEQUENCES: 552
                                                                                                                                                                                                                   ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
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APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
Sequence*180, Application US/08858207A Patent No. 6348328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P50475
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APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 180:
SEQUENCE CHARACTERISTICS:
LENGTH: 836 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
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425.00
76.35%
56.08%
18.69%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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CLASSIFICATION:
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Best Local Similarity:
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Pred. No.:
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259 AlaAlaLeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGlu 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLeuLysGluValLysGluIleAlaLys-------ProAsnGluIle 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 AspGlnLeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGly 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----MetAlaSerArg 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleLeuGlyMetGlyAspValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGln 314
                                                                                                                                                                                MetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLysLeuAlaLeuLeu 124
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685 GCTATIGAICAATIGAAGTITIGGGGCGAAGGTGTTGGTGTAGATGTAATIAGCCAAAGT 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TTAATCACTGCAGACGTCGGTTTTAAT 399
                                                              ----ATGACGTTAACTGAAGAATTACGTATGGAAGCACAACGACGT 447
                                                                                                                   -----AsnThrSerIleAsnMetSerAsnLysProProThrValVal 104
                                                                                                                                                                                                                                           125 MetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspIleTyrArgProAla 144
                                                                                                                                                                                                                                                                                                    145 AlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProValTyrSerGluGly 164
                                                                                                                                                                                                                                                                                                                                                                                                               165 AspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAlaLysGluGluHis 184
                               48 ValValLysGluPheIleLysThrValSerGluArgAlaLeuGlySerAspValMetGln 67
                                                                                              68 SerLeuThrProGlyGlnGlnValIleLysIleValGlnAspGluLeuThrLysLeuMet 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 LysLeuAspGlyLeuGluLeuPheHisProGluArg--
349 IIIIIIGAAGCIIIAGAAGAAAIG-----
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Search completed: February 25, 2003, 03:14:46 Job time : 109 secs

Sequence 37, Appl Sequence 1847, Ap Sequence 9156, Ap Sequence 9427, Ap Sequence 1, Appli

OM protein

Run on:

Sequence:

Title: Perfect

Searched:

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APELICANT: CITT, Grant J.
APELICANT: Tamamorto, Robert T.
APPLICANT: Yamamorto, Robert T.
APPLICANT: Yamamorto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKARYOTES
FILE REPERBNCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-03-23
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
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US-09-815-242-2506

US-09-736-475-1094

US-09-902-941-1094

US-09-902-941-1094

US-09-849-626-1094

US-09-849-626-11494

US-09-960-352-114727
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0. US-09-815-242-1949

0. US-09-815-242-6868

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0. US-09-815-242-6991

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0 US-09-815-242-6764
0 US-09-09-27A.37
0 US-09-974-300-1847
0 US-09-815-242-9156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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US-09-815-242-8968
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-MODEL_frame+_pzn.model_DEV=xlp
-MODEL_frame+_pzn.model_DEV=xlp
-MODEL_frame+_pzn.model_DEV=xlp
-MODEL_frame+_pzn.model_DEV=xlp
-MODEL_frame+_pzn.model_DEV=xlp
-MODEL_frame+_pzn.model_DEV=xlp
-MODEL_frame+_pzn.model_DEV=xlp
-DE=bublished_Applications_NA -QFWT=fastap -SUFFIX=rpb -MINNATCH=0.1
-LOOPCL_0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=cr THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=cxt -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -GSER=US09943108_GCGN_1_1_80_erunat_21022003_151633_1953
-NCPU-STAY -NO_MARP -LARREDGURY -NORM=CXT -HEAPSIZE=500 -MINLEN=0
-DEV_INROUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -TGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 4365, Ap
Sequence 8030, Ap
Sequence 3890, Ap.
                                                                                                                                                                                                                                            (without alignments)
2871.303 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                   US-09-943-108A-2
2274
1 MAFEGLSERLQATMQKMRGK.......GKKGKRNQMQNMLKGMNLDF 455
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/cgn2_6/ptodata/1/pubpna/DSO7_BNEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/NSO6_BNEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_BNEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_BNEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_BNEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
                                  GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                     - nucleic search, using frame_plus_p2n model
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US-09-815-242-4365
US-09-815-242-8030
US-09-815-242-8990
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Database

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Sequence 38, Appl Sequence 13494, A Sequence 14727, A

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LeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAla
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Patent No. US20020061569A1
: APPLICANT: Haselbeck, Robert
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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US-09-815-242-4365
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8968
LENGTH: 1368
                                                                                                                                                                                                                                    Indels:
                                                                                             TYPE: DNA ORGANISM: Staphylococcus aureus
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2261.00
99.78%
99.34%
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US-09-815-242-8968
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                                                                                                                               NAME/KEY: CDS
LOCATION: (1).
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APPLICANT. SUMMER: ON THE CASE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROCRATYOUS
FILE REPRENCE: ELITRA.011A
CURRENT APPLICATION UNMER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,737
PRIOR APPLICATION NUMBER: 60/207,737
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PRIOR APPLICATION NUMBER: 60/207,737
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                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                   Length:
Matches:
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SEQ ID NO 4365
; SEQ ID NO 4365
; TPRE: DNA
                                                                              ; ORGANISM: Staphylococcus aureus
US-09-815-242-4365
                                                                                                               4.42e-242
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98.24%
98.28%
                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                          Alignment Scores:
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CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 66/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-33
PRIOR PELICATION NUMBER: 60/242/578
PRIOR PILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/253/625
PRIOR PELICATION NUMBER: 60/253/931
PRIOR PELICATION NUMBER: 60/253/931
PRIOR PELICATION NUMBER: 60/257/931
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TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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NUMBER OF SEQ ID NOS: 14110

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RESULT 4
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Matches:
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                             TYPE: DNA ORGANISM: Staphylococcus aureus
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Query Match:
SOFTWARE: FastSEQ
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Wall, Daniel
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APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Vanamoto, Robert T.
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                     ) ORGANISM: Enterococcus faecalis US-09-815-242-3890
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ACCGATITAGAAATITICCATCCCGATCGTATGTCGAGTCGTATCCTAGGTATGGGGGAC 900
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PILICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
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PRIOR PELING DATE: 2000-02-16
NUMBER OF SED IN NOS: 14110
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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Zyskind, Judith
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Mismatches:
Indels:
                                                                                                                Length:
Matches:
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                                  ORGANISM: Enterococcus faecalis
                                                                                                              3.23e-150
1418.50
77.54%
58.96%
62.38%
                                                                   ...(1434)
                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                     ; LOCATION: (1).
US-09-815-242-6764
                                                         NAME/KEY: CDS
                                                                                                      Alignment Scores:
O ID NO 6764
LENGTH: 1434
                        TYPE: DNA
                                                FEATURE:
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TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
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                                                 281 AspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAsp
                                                                              841 ACCGATTTAGAAATTTTCCATCCCGATCGTATGTCGAGTCGTAGGTATGTAGGGGAC
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <UNKNOWN>
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APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
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STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/09070927A Patent No. US20020120116al GENERAL INFORMATION:
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Patrick J. Dillon
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Mismatches:
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                                                                                                                                                                                                                                                                 ength:
                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                         NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
APPLICATION NUMBER: 60/066,009 FILING DATE: 1997-11-14
                                                                                            TELEPHONE: (301) 309-8504
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                   TELECOMMUNICATION INFORMATION:
                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                              3.83e-149
1417.50
77.54%
58.96%
62.34%
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Best Local Similarity:
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                                                                                                                                 LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu
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Ratent No. US20020146721A1
GENERAL INFORMATION
FEBREAL INFORMATION
FEBREAL OF INVENTION BATHOGS FOR MATHOGS FOR MATHOGS FOR MATHOGS FOR MATHOGS FOR MONITORING MULTIPLE OF INVENTION: MATHOGS FOR MONITORING MULTIPLE OF INVENTION: EXPRESSION
FILE REFRENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 60/29,526
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-03-27
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SOFTWARE: FastSEQ for Windows Version 4.0
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GAGCAAAAAATGAAAAATATGAGCTTTACGCTCGACGACTTTTTGGAACAGCTCGGACAG 1020
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1 MetalaPheGluGlyLeuSerGluArgLeuGlnAlaThrWetGlnLysMetArgGlyLys
                                               GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln
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Mismatches:
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Matches:
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APPLICANT: Trawick, John D.
APPLICANT: Tamancto, Robert T.
APPLICANT: Tamancto, Robert T.
APPLICANT: Tamancto, Robert T.
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Prokaryotes
FILE RFERENCE: ELITRA, 011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-28
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SUPPLING DATE: 2001-02-16
                                                                                                                                                                                                                                                               Sequence 9156, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Streptococcus pneumoniae
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1307.00
74.73
55.128
57.488
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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US-09-815-242-9156
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Best Local Similarity:
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                                                                                                                                                                                                                                  RESULT 8
US-09-815-242-9156
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                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                            1.66e-148
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87.30%
71.43%
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Best Local Similarity:
JS-09-974-300-1847
                               Alignment Scores:
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NVENTION: METHODS USING THE SRP POLYNUCLEOTIDES
WYENTION: AND POLYPEPTIDES COMPOUNDS MODULATING THEIR ACTIVITY
ENCE: GMSGONES: US/09/814,041A
LING DATE: 2001-03-20
ICATION NUMBER: 60/191,008
NG DATE: 2000-03-21
SEQ ID NOS: 2
FESTSEQ for Windows Version 4.0
spMetLysLysMetMetLysGlnPheThrGlyGlyGlyLysGlyLysLysGlyLys 440
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                                                                                                                                     snGlnMetGlnAsnMetLeuLysGlyMet------AsnLeuPro 454
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Matches:
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                                                       TyrargproalaalalleasnGlnLeuGlnThrValGlyLysGlnIleaspIleProVal 160
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LeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAlaAspile 140
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                                                                                       TATCGTCCAGCTGCCATTGACCAGCTTAAGACCTTGGGACAACAGATTGATGTGCCTGTC 480
                                                                                                                    TyrSerGluGlyAspGlnValLySProGlnGlnIleValThrAsnAlaLeuLySHisAla 180
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; Sequence 2255, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INPORMATION:
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ValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrThrAlaGlyLysLeuAla 122
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Conservative:
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Indels:
                                                                                                                                                            TITLE OF INVENTION: NOVEL POLYNOLEGYIDES
TILE REFERENCE: 249-125
CURRENT PEPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PLICATION NUMBER: JP 99/377484
PRIOR PLILNG DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEO ID NOS: 7059
SOFTWARE: PETENTIN VET: 3.0
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NAKAGAWA, SATOSHI
MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                               HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                     OZAKI, AKIO
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Best Local Similarity:
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LENGTH: 1641
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GlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAlaLysGluGluHisLeu 185
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                            ------CCAGTCGAGGTAGCGCGCGCGGTATCGAAGAAGCCAAGCGCACCCAGCAC
                                                           186 AspPheValileileAspThrAlaGlyArgLeuHisIleAspGluAlaLeuMetAsnGlu
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Oblesen, Rai L.
APPLICANT: Zyskind, Judith W.
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103 ValValMetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLysLeuAla 122
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                                                                                                                       in
                                              APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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Mismatches:
Indels:
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Matches:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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1164.50
71.74%
50.99%
51.21%
Wall, Daniel
Trawick, John D.
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Best Local Similarity:
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US-09-815-242-6166
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Pred. No.:
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LENGTH: 1362
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                                                                                                                                                                                                                                                                                                                                                                           LeuGluLeuPheHisProGluArgMetAlaSerArgIleLeuGlyMetGlyAspValLeu 302
                                                                                                        GluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGluAlaLeu 202
                                                                                                                                                           MetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeuValVal 222
                                                                                                                                                                           AspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeuAsp 242
ProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProValTyrSer 162
                         CCGCCGCCAATCAAACACCTTGAGACGCTGGCAGAGCAGGTGGGCGTTGATTTCTTCCCT 483
                                                   GluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAlaLysGlu 182
                                                                                                                                                                                                                              SerLeulleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeuGluLys
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                                                                             184 TCTGATGTTGGTCAGAAGCCGGTAGATATCGTTAACGCGGCGCTGAAAGAAGCCAAACTG
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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US-09-815-242-1949/c
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                                         APPLICANT: YanamorCo, Mobert T.
APPLICANT: YanamorCo, Mobert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROCARTYOTES
FILE REFERENCE: ELITEA.011A
CURRENT PELING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-11-27
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 1949
LENGTH: 721
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Matches:
Conservative:
Mismatches:
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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1158.00
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Best Local Similarity:
Query Match:
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                                APPLICANT:
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LysasnLeuGlyProLeuaspaspIleMetLysMetIlePro------GlyMetasn 358
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                                                                                                                                                                                                                                                                                                                                                                                                       ProAlaAlaIleAsnGlnLeuGlnThrValGlyLySGlnIleAspIleProValTyrSer 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAlaLysGlu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 TCCGACGTCAGCCAGAAGCCGGTGGCCATCGCCGAGGCGGCGATCCGCGAGGCGAGGCTG 543
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                          64 CTGACCGAGGACAACATCTAGCGCGAAGTGCGCATGGCCTTGCAGGCC 123
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                                                                                  IleargSerValThrGlnLySProIleLySPheValGlyMetSerGluLySLeuAspGly
   LeuThrGluAlaAspIleLysIleMetMetArgGluValArgLeuAlaLeuPheGluAla
                                                                                                                                  SerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleValGlnAspGlu
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Mismatches:
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PRICR APPLICATION NUMBER: 60/191,078
PRICR FILING DATE: 2000-03-21
PRICR FILING DATE: 2000-05-21
PRICR FILING DATE: 2000-05-23
PRICR FILING DATE: 2000-05-26
PRICR PRICR APPLICATION NUMBER: 60/207,727
PRICR FILING DATE: 2000-10-23
PRICR FILING DATE: 2000-10-23
PRICR FILING DATE: 2000-11-27
PRICR FILING DATE: 2000-11-27
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PRICR FILING DATE: 2000-12-25
PRICR FILING DATE: 2000-12-25
PRICR FILING DATE: 2000-12-25
PRICR FILING DATE: 2000-12-25
PRICR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 7850
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Boward
TITLE OF INVENTION: Identification of Essent
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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APPLICANT: Haselbeck, Robert
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US-09-815-242-7850
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US-09-815-242-7850
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APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carry Grant J.
APPLICANT: Carry Grant J.
APPLICANT: Au, H. Howard
TILE OF INVENTION: Deckaryotes
FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: 05/09/815,242
CURRENT APPLICATION NUMBER: 60/11,078
FRIOR FILING DATE: 2001-03-21
FRIOR PELICATION NUMBER: 60/206,848
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
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Conservative:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6868
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6868, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Haemophilus influenzae
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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70.67%
50.00%
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APPLICANT: Haselbeck, Robert
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Best Local Similarity:
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US-09-815-242-6868
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Query Match:
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Db 1144 TCCATGACCCTAAAAGAACGTGCCAACCCAGATATTATCAA.  Qy 402 IlealaLysGlySerGlyArgSerLeuGlnGluValasnar.	1144 TCCATGACCCTAAAAGAACGTGCCAACCCAGATATTATCAAAGGATCTCGCCGTCGTCGT 1203	IlealaLysGlySerGlyArgSerLeuGlnGluValAsnArgLeuWetLysGlnPheAsn 421	ATTGCATTAGGCTCTGGCACTCAAGTGCAAGATGTCAATAATTACTTAAACAATTGGAT 1263	hrGl	::: AAAATGCGTAAAGGCGGC 1302	LysGlyMet 451	:::	2003, 04:03:39
arc	. TCCATGACCCTAAAAGAACGT	IlealaLysGlySerGlyArg	ATTGCATTAGGCTCTGGCACT	2 AspMetLysLysMetMetLys	GAAATGCAACGTATGATGAAG	AsnGlnMetGlnAsnMetLeu		<pre>mpleted: February 25, : 113 secs</pre>
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February 21, 2003, 15:16:32 ; Search time 22 Seconds (without alignments) 1988.235 Million cell updates/sec
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1 MAFEGLSERLQATMQKMRGK......GKKGKRNQMQNMLKGMNLPF 455
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Description	hypothetical protesignal recognition signal recognition
SUMMA	H88896 A11299 A414571 B414571 B414571 B83960 H88826 H88216 B9017 F792149 A10633 B61033 B61063 B61063 B61063 B61792 B61792 B61792 B61792 B61792 B61792 B61792 B61792 B61793
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AD3280	F90554	S36637	G82851	E70448	H84975	F97726	C87702	A71728	S35481	C82936	E70186	C64205	S73419	C81718	D71566
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523	449	564	434	454	451	449	508	449	447	448	447	446	450	448	448
46.4	46.2	45.0	44.8	44.4	44.2	43.2	42.7	42.2	41.5	41.1	39.8	39.5	39.4	39.1	38.2
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## ALIGNMENTS

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Signal recognition particle chain ffh - Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Sate: 16-F9b-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C; Accession: B47154, R69621
R; Honda, K.; Nakamura, K.; Nishiguchi, M.; Yamane, K.
J. Bacteriol. 175, 4865-4894, 1993
A; Fitle: Cloning and characterization of a Bacillus subtilis gene encoding a homolog A; Reference number: A47154; MUID:93328695; PMID:8335643
A; Accession: B47154
A; Status: preliminary
A; Molecule type: nucleic acid
A; Residues: 1-446 < GNON
A; Cross-references: GB:D14356; NID:9439700; FIDN:BAA21691.1; FID:92309080
A; Cross-references (B:D14356; NID:9439700; RUBN:135652, NCBIF:135654)
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be
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Web.
                                F.; Berche, P.; Bloe
; Entian, K.D.; Fsih
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Voss, H.; W
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-450 cGLA>
A; Cross-references: GB: AL592022; PIDN: CAC97145.1; PID: g16414416; GSPDB: GN00178
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                      Ridlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Be.; Domiquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; John C.; Schlueter, T.; Simces, N.; Teirrez, A.; Vazquez-Boland, J.A.; A; Reference number: ABIO77; MUD:21537279; PMID:11679669
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Fitle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
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C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
                                                                                                                                                                                                                                                                                 signal recognition particle protein Ffh homolog ffh [imported] - Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                               C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AI1299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
   KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRIMKQF 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.5%; Score 1717.5; DB ilarity 72.7%; Pred. No. 1.6e-80; Conservative 64; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   450
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                                                             NDMKKMMKQFTGGGKGKKKKRNQMQNMLKGMNLPF 455
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A) Cross-references: GB:NC_003210; PI
A) Experimental source: strain EGD-e
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Rivolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacteria A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Status: preliminary
                                                                                A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06203.1; GSPD3 A;Experimental source: strain C-125 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal recognition particle GTPase Ffh [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: E97116
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A:Rossidues: 1-449 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK79720.1; PID:g15024723; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
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Pred. No. 5.4e-64;
                                                                                                                                                                                                                                              Query Match 69.7%; Score 1584; DB 2; Length 451; Best Local Similarity 67.3%; Pred. No. 1e-73; Matches 307; Conservative 73; Mismatches 70; Indels
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                                                                                                                                                                A;Gene: ffh
C;Superfamily: signal recognition particle 54K protein
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Matches 280; Conservative
                                      A; Molecule type: DNA
A; Residues: 1-451 <STO>
             Status: preliminary
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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Natures 390, 249-256, 1997
A. Mathors: Foulger, D.; Eritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogi, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Latadinois, A.; Authors: Lauber, J.; Lazarevic, V.; Eckee, S.M.; Evine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron akenchi, M.; Tamakoshi, A.; Taraka, T.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Vohiyama, T.; Winters, P.; Wipat, A.; Tanako, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Hitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Reference number: A69580; MUID:98044033; PMID:9384377
A.; Residues; 1-446 < KUND.
A.; Residues: 1-446 < KUND.
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A;Experimental source: strain 168
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Recession: D83960
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C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002
C;Accession: D83960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LALIAMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420

    GODVMKSLTPGQQVIKVVQEELTELMGGEESKIAVAKRPPTVIMMVGLQGAGKTTTSGK 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAFEGLADRIQQTISKIRGKGKVSEQDVKEMMREVRLALLEADVNFKVVKDFVKKVSERA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.4%; Score 1647; DB 2; Length 446; larity 70.1%; Pred. No. 6.2e-77; Conservative 66; Mismatches 60; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: signal recognition particle 54K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDMKKMMKQFTGGGKGKKGKRNQMQNMLKGMNLPF 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEMKKMMKQMTNMSKGKK-----KGFKLPF 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 319; Conserv
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Matches
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Db 241 LDITGVIITKLDGDTRGGAALSIREITGKPIKFTGTGEKLTDLEVFYPDRMSSRILGMGD 300  Qy 301 VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGHNKM 360  :::       :::      :::  :      ::	RESULT 8  By 1917  By 1920-1918  By 1917  By 1920-1919  C; Species: Streptococcus pneumoniae (strain R6)  C; Species: Streptococcus pneumoniae  C; Accession: E98017  R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.*  F; Sun, P.M.; Winkler, M.E.  J; Bacteriol. 183, 5709-5717, 2001  A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.  A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  A; Reference number: A97872; MuID:21442945; PMID:11544234  A; Recession: E98017  A; Residues: 1-523 < KGUR>  ; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 < KGUR> A; Residues: 1-523 <	QUETY MATCH  QUETY MATCH  Best Local Similarity 55.1%; Proc. 1307; DB 2; Length 523;  Matches 283; Conservative 90; Mismatches 102; Indels 14; Gaps 2;  QY I MAFEGLERLQATMQKMRGKGKLTEADIKIMAREVRLALFEADVRFVVKEPIKTVSERA 60	Db 12
Db   MAPEGLSTKLQAAMKKLRGKGKLSEKDIKDAMREVKLALLEADVNYKIVKNFVKVVGEKC 60	QY 241 LDVTGVTLFKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300  ::	C; Accession: H86826 R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001 A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss A; Reference number: A86625; MUD:21235186; PMID:11337471 A; Reference number: A86625; MUD:21235186; PMID:11337471 A; Redession: H86826 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-518 A; Residues: 1-518 A; Residues: 1-518 A; Cross-references: G** A** CROOP A; Cross-references: G** A** CROOP A; Cross-references: G** A** CROOP A; Cross-references: G** A** CROOP A; Cross-references: G** A** CROP A; Cross-references: G** A** CROP A; Cross-references: G** CROP A; Cross-references:	Query Match 57.8%; Score 1315; DB 2; Length 518; Best Local Similarity 55.4%; Pred. No. 6.1e-60; Matches 258; Conservative 88; Mismatches 102; Indels 18; Gaps 2; Qy 1 MAFEGLSERLQATWQKMRGKGKLTEADIKINMREVRLALFEADVNFKVVKEPIKTVSERA 60 1

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5,

Gaps 62 61

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signal recognition particle protein [imported] - Salmonella enterica subsp. enteric (Species: Salmonella enterica subsp. enterica serovar Typhi A; Mote: this species has also been called Salmonella typhi (C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 (C; Accession: Ai0833 R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Chur th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fa Nature 413, 846-852, 2001 A; Muther 51, O'Gaora, P. Nature 413, 846-852, 2001 A; Muther 51, O'Gaora, P. Nature 413, 846-852, 2001 A; Muther 51, O'Gaora, P. Nature 413, 846-852, 2001 A; Muther 51, O'Gaora, P. Nature 413, 846-852, 2001 A; Muther 51, O'Gaora, P. Nature 413, 846-852, 2001 A; Muther 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P. Nature 51, O'Gaora, P
                                                                                                                                                          GB:AE000512; NID:94982133; PIDN:AAD36632.1; PID:94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 VTGVILTKIDGDTRGGAALSIRSVTQKPIKFVGMSEKIDGLELFHPERMASRILGMGDVL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 SLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKMKG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 LDKI,NMSEKQIDHIKAIIQSMTPAERNNPDTLNVSKKKRIAKGSGRSLQEVNRLMKQFND 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 SDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMAYGLQGAGKTTTAGKLA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 FEGLSERLQATMOKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99; Indels
                      A) Status: preliminary
A) Molecule type: DNA
A) Residues: 1-433 - 430.
A) Cross-references: GB: ABC01802; GB: AEC00512; NID: 94982
A) Experimental source: strain MSB
A) Genelics:
A) Genelics: TM1565
C) Superfamily: signal recognition particle 54K protein
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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; Pred. No. 3.4e-53
92; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                          53.48;
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Best Local Similarity 53.4%
Matches 234; Conservative
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A; Accession:
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A;Gene: STY
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hickey
on, D.;
                                                                                                                                                                                                                                   C, Accession: F95149

R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A, Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A, Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Residues: 1-523 <RUR>
A.Cross-references: GB:AE005672; PIDN:AAK75391.1; PID:g14972772; GSPDB:GN00164; TIGR:SP4
                                                                                                                      signal recognition particle protein [imported] - Streptococcus pneumoniae (strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signal recognition particle protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: F72236
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                    C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #seguence_revision 03-Aug-2001 #text_change 17-May-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.4%; Score 1306; DB 2;
54.9%; Pred. No. 1.8e-59;
ive 91; Mismatches 102;
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Matches 252; Conservative
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                                                    LLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKE
                                                                                     122 KFIREKHKKKVLVVSADVYRPAAIKQIETLAEQVGVDFFPSDVGQKPVDIVNAALKEAKI
                                                                                                                       EHLDFVIIDTAGRIHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD
                                                                                                                                                                                          243 VTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVL
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A;Molecule Type: DM.
A;Residues: 1-453 <BLAT>
A;Residues: 1-453 <BLAT>
A;Cross-references: GB:AE000347; GB:U00096; NID:q2367142; PIDN:AAC75659.1; PID:g1788963;
A;Experimental source: strain K-12, substrain MG1655
EMBO J. 2, 899-905, 1983
EMBO J. 2, 899-905, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The nucleotide sequence of an Escherichia coli operon containing genes for the A;Reference number: A30380; MUID:84057772; PMID:6357787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signal recognition particle protein - Escherichia coli (strain K-12)
(S.psecies: Escherichia coli
(S.psecies: Escherichia coli
(S.psecies: Escherichia coli
(S.psecies: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
(S.Accession: E65039; S07178
(S.A.) Rose, P. Bunkert III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Science 277, 1453-1462, 1997
(Science 277, 1453-1462, 1997
(A.Reference number: A64720; MUID::97426617; PMID::9278503
(A.Reference number: A64720; MUID::97426617; PMID::9278503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL:X01818; NID:g43141; PIDN:CAA25957.1; PID:g43142
                                                                                                                                                                                                                                           SDVMQSLIPGQQVIKIVQDELfKLMGGENTSINMSNKPPTVVMMYGLQGAGKTTTAGKLA
                                                                                                          HEVNKSLTPGQEFVKIVRSELVAAMGEENQTLNLAAQPPAVVIMAGLQGAGKTTSVGKLG
                                                                                                                                                                                                                                                                                                                                                                                              SLIEDIESKVDRAQAEKLATKLKKGDGFDLNDFLEQLKOMKNMGGMASLMGKLPGMGQIP
                FEGLSERLQATMOKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG
                                                                                                                                                                                                                       EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD
                                                                                                                                                                                                                                                                                          VTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1164.5; DB 2;
Pred. No. 2.4e-52;
4: Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DMKKMMKQFTGGGKGKKGKRNQMQNMLKGMNLP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DMORMMK-----KMKKGGMAKMMRSMKGMMPP 448
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51.0%;
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A; Residues: 86-453 <BYS>
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Best Local Similarity
Matches 231; Conserv
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signal recognition particle protein VC0560 [imported] - Vibrio cholerae (strain N16 C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82300
R;Heidelberg, J.F.: Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Selle 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUD:20406833; PMID:10952301
A;Ctaus: preliminary
A;Molecule type: DNA
A;Residues: 1-461 - (HEL)
A;Cross-references: GB:AE004142; GB:AE003852; NID:99554988; PIDN:AAF93728.1; GSPDB: A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 VIGVILIKLDGDTRGGAALSIRSVIQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVL 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 EHLDFVIIDTAGRIHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 FEGLSERLOATMOKWRGKGKLTBADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 50.6%; Score 1150.5; DB 2; Length Best Local Similarity 50.8%; Pred. No. 1.2e-51; Matches 228; Conservative 91; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1
C;Superfamily: signal recognition particle 54K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February 21, 2003, 15:19:26
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A;Molecule type: DNA
A;Residues: 1-453 <STO-
A;Residues: 1-453 <STO-
A;Cross-references: GB:AE005174; NID:g12517035; PIDN:AAG57721.1; GSPDB:GN00145; UWGP:239
A;Experimental source: strain 0157:H7, substrain EDL933
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                                                                                        GLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQFN 421
                                                                                                                                362 DNVKSQMDDKVLVRMEAIINSMTMKERAKPEIIKGSRKRRIAAGCGMOVQDVNRLLKOFD 421
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          SLIEKAQQDVDQEKAKDLEKKMRE-SSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKMK 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.2%; Score 1164.5; DB 2; Length Best Local Similarity 51.0%; Pred. No. 2.4e-52; Matches 231; Conservative 94; Mismatches 121; Indels
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421

RESULT 15

5

Gaps

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Length 461;

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: February 21, 2003, 15:13:26; Search time 14 Seconds (without alignments)

1347.981 Million cell updates/sec

1 GS-09-943-108A-2

Perfect score: 2274

1 MAFEGLSERLOATMOKMRGK......GKKGKRNOMONMLKGMNL,PF 455

Scoring table: BLOSUMG2

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892
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Database : SwissProt\_40:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P37105 bacillus su Q54431 streptococc P07019 escherichia P4418 streptococc Q10196 sucherichia P4418 synechococc Q10963 mycobacteri Q55311 synechococc Q10963 mycobacteri Q57107 arabidopsis O67615 aquifex aeo P57473 buchnera ap Q07615 aquifex aeo P57473 buchnera ap Q07615 mycoplasma P75054 rhermus aqu Q92424 mycoplasma P75054 mycoplasma P75054 mycoplasma P75056 methanococc Q07853 sulfolobus Q9776 pyrococcus Q5736 methanobact Q59307 pyrococcus Q59307 pyrococcus Q97267 methanobact Q9633 archaeoglob Q97267 methanobact Q9633 archaeoglob Q97267 thermoplasm Q97948 thermoplasm Q97948 thermoplasm Q97948 thermoplasm Q97948 taacharopycoppersico P20424 saccharomyc
qi	SR54_BACSU SR54_STRMU SR54_STRMU SR54_STRMU SR54_STRW1 SR54_STRW1 SR54_STRW1 SR54_STRW1 SR54_STRW1 SR54_MYCTU
Length DB	$\begin{array}{c} 4\Omega  4444  400  000  4444 $
ry	7.7.0.0.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.
Ö	11123.5 111123.5 111123.5 11103.5 11103.5 11103.5 11006.5 11006.5 1006.5

	P49968 hordeum vul	P21565 schizosacch	P49969 hordeum vul	P13624 homo sapien	P14576 mus musculu	P49966 arabidopsis	015821 entamoeba h	P49970 hordeum vul	Q00179 aspergillus	042816 candida alb	Q99150 yarrowia li
SR51_LYCES	SR51_HORVU	SR54_SCHPO	SR52_HORVU	SR54_HUMAN	SR54_MOUSE	SR52_ARATH	SR54_ENTHI	SR53_HORVU	SR54_ASPNG	SR54_CANAL	SR54_YARLI
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496	497	522	497	504	504	495	487	493	534	556	536
27.1	27.1	27.1	27.1	27.1	26.9	26.8	26.6	26.5	25.8	25.6	25.1
617	617	617	616	615.5	612.5	609.5	605	602.5	586	582	571
34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

DESCUT. 1  SR54_BACSU  DE SAFABEACSU STANDARD; PRI; 446 AA. BACSU  DT 01-OCT-1994 (Rel: 30, Created)  DT 01-OCT-1994 (Rel: 30, Last sequence update)  DT 01-OCT-1994 (Rel: 30, Last sequence update)  DT 15-JUN-2002 (Rel: 41, Last annoctation update)  DE Signal recognition particle protein (Fifty-four FFH)  SEQUENCE FROM N.A.  RACINES STAIN-168; Bacillales; Bacillaceae; EX NCBL-TAXID-4123;  RA MEDINE-9328065; PubMed-8335643;  RA MEDINE-9328065; PubMed-8335643;  RA MEDINE-9328065; PubMed-8335643;  RA MEDINE-9328065; PubMed-8335643;  RA MEDINE-9328065; PubMed-9384377;  RA MINE-EROM N.A.  RA MEDINE-9328065; PubMed-9384377;  RA MINE-18 R., Relander L., Rabbet L., Rebret C., Reiral E., Britan K.D., Eriphton J., Rabbet C., Reiral E., Rabbet C., Redin S., Golizar R. Allbert H., Holsappel S., Hosono S., Hullo M.P.  RA MINE K., Lapidus A., Liu H., Masune C., Reiral E., Rabbet C., Roche E., Rabane R., Ya Sekuyaka A., Serror P. R. Arendal M., Mendler H., Yannaer F. R. Arendal M., Panlander R., Yannaer C., Rolldaw R., Sernor P. R. Arendal M., Panlander R., Yannaer C., Rochidaw H.F., Zunatenle B., Yannaer F., Rabenchi M., Tanakoshi A., Tanahoshi B., Tanakoshi A.,	D; PRT; 446 AA Created)  Last sequence update) Last sequence update) Last sequence update) Last sequence update Licle protein (Fifty- Last annotation updat Licle protein (Fifty- Mishiguchi M., Yaman Lization of a Bacillus acali Ffh."; ABSSELT, Albertin G., Bessieres P., Bol C. V. Caldwell B., Can dia coli Ffh."; ABSSELT, Albertin G., Bessieres P., Bol C. V. Caldwell B., Can C. V. Caldwell B., Can C. V. Caldwell B., Can C. V. Caldwell E., Can G. Connerton I.F., Cum G., Bessieres P., Bol C. V. Caldwell B., Can Goffeau A., Enter Julita T., Fuma S., Ga Goffeau A., Galightiy Asabata Y., Klaerr P., Mizuno M., Weestl Ogawa K., Ogiwara A., Ostretelle D., Porwoll Ogawa K., Ogiwara A., Ostretelle D., Porwoll Ostretelle D., Porwoll Purnelle B., Napopor Rocha E., Roche B., Contetelle B., Roche B., A., Seror S.J., Seri A., Tanaka T., Tarbas A., Tanaka T., Tarbas A., Tanaka T., Tarbas A., Tanaka T., Tarbas A., Tanaka T., Tarbas A., Tanaka T., Yamamot H., Yamane K H.F., Zumstein E., Yon Gudler H., Yamane K H.F., Zumstein E., Yon Gudler H., Yamance Of the Gram F 77).	PRICE BACKSU STANDARD; PRT; 446 AA.  1971.  1971.  1971.  1071.
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                    Gutierrez J.A., Crowley P.J., Brown D.P., Hillman J.D., Youngman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus mutans by using transposon Tn917: preliminary characterization of mutants displaying acid sensitivity and nutritional requirements.";
J. Bacteriol. 178:4166-4175(1996).
-:- FUNCTION: NECESSARY FOR BFFICIENT EXPORT OF EXTRA-CYTOPLASMIC PROYENS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMBRGES FROM THE RIBOSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBUNIT: SIGNAL RECCGNITION PARTICLE CONSISTS OF A SWALL CYTOPLASMIC RNA (SC-RNA) MOLECULE AND PROTEIN FFH.
-:- DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                         -! - SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                       301 VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bleiweis A.S.; "Insertional mutagenesis and recovery of interrupted genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gutierrez J.A., Cvitkovitch D.G., Brady L.J., Hamilton I.R., Hillman J.D., Bleiwais A.S.;
Hillman J.D., Bleiwais A.S.;
"Fth of Streptococcus mutans is involved in acidurance.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Signal recognition particle protein (Fifty-four homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                NDMKKMMKQFTGGGKGKKGKRNQMQNMLKGMNLPF 455
                                                                                                                                                                                                                                                                                                                                         516 AA.
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Interpro; IPR004125; SRP54_SPB.
Interpro; IPR004780; SRP24b.
Pfan; PF00448; SRP54; 1.
Pfan; PF02881; SRP54_N; 1.
                                                                                                                                                                                                                                                                                                                                                         054431; P96469;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence)
16-OCT-2001 (Rel. 40, Last and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U88582; AAB48050.1; -. EMBL; U48883; AAC44500.1; -. HSSP; O07347; ZFFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-142 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus.
NCBI_TaxID=1309;
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                                                   Nakamura K., Nishiguchi M., Honda K., Yamane K.; "The Bacillus subtilis SRP54 homologue, Ffh, has an intrinsic GTPase activity and forms a ribonucleoprotein complex with small cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Indels 10; Gaps
                                                                                                             RNA in vivo.";
Biochem. Biophys. Res. Commun. 199:1334-1399(1994).
-!- FUNCTION: NECESSARY FOR BEPICTENT EXPORT OF EXTRA-CYTOPLASMIC
-!- PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE
                                                                                                                                                                                                                                                                DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN
BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 KEEHYDYVILDTAGRLHIDHELMDELTNVKEIANPEEIFLVVDSMTGQDAVNVAKSFNEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA
                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00382; AAA; 1.
TIGREMBS, TIGREMOS95; 3a0501s01; 1.
PROSITE; PS00300); SREP4; 1.
Signal recognition particle; GTP-binding; RNA-binding; Membrane;
                                                                                                                                                                                                        -:- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A SMALL CYTOPLASMIC RNA (SC-RNA) MOLECULE AND PROTEIN FFH.
-: SUBCELLUTAR LOCATION: Membrane-associated.
-:- DOMAIN: THE RROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.4%; Score 1647; DB 1; Length 446; 70.1%; Pred. No. 2.1e-78; ive 66; Mismatches 60; Indels 10
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M-DOMAIN (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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HSSP; 007347; IFFH.

Subtilist; B6710830; ffh.

InterPro; IPR0003593; AAA_ATPase.

InterPro; IPR000897; SRP54.

InterPro; IPR004125; SRP54_SPB.

InterPro; IPR004125; SRP54_SPB.
[3]
CHARACTERIZATION.
MEDLINE=9419773; PubMed=7511896;
MEDLINE=9419773: Menda
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191 195 GTI
249 252 GTI
446 AA; 49541 MW; I
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Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDom; PD000819; SRP54; 1.
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NP_BIND
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Page 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::||:|||::|| ::||::|| 361 PALANVEVDEGEIARKRAIVSSMTPEERENPDLLITPSRRRRIASGSGNTFVNVNKFIKDF 420
                                                                                                                                                                                                                                                  LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-8405772; PubMed=6357787;
Bystroem A.S., Hjalmarsson K.J., Wikstroem P.M., Bjoerk G.R.;
Bystroem A.S., Hjalmarsson K.J., Wikstroem P.M., Bjoerk G.R.;
Bystroem A.S., Hjalmarsson K.J., Wikstroem P.M., Bjoerk G.R.;

Bystroem A.S., Hjalmarsson K.J., Wikstroem P.M., Bjoerk G.R.;

genes for the tRNA(mlG)methyltransferase, the ribosomal proteins S16 and L19 and a 21-K polypeptide.";

EMBO J. 2:899-905(1983).
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                  1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SR54_ECOLI STANDARD; PRT; 453 AA.
P07019; P77007; P77008;
01-APR-1986 [Rel. 07, Created)
01-JNN-1990 [Rel. 13, Last sequence update)
15-JUN-2002 [Rel. 41, Last annotation update)
Signal recognition particle protein [Fifty-four homolog) [P48].
PFH OR B2610 OR E3994 OR ECS3473.
Escherichia coli, and
Escherichia coli 0157:H7.
                                                                                                                                                                             10;
                                                                                                                                                     DB 1; Length 516;
                                                                                                                                                                             Indels
                                           Signal recognition particle; GTP-binding; RNA-binding.

DOMAIN 297 516 G-DOMAIN (BY SIMILARITY).

NP_BIND 108 115 GTP (BY SIMILARITY).

NP_BIND 191 195 GTP (BY SIMILARITY).

CONFLICT 49 252 GTP (BY SIMILARITY).

CONFLICT 49 49 V -> A (IN REF. 2).

SEQUENCE 516 AA, 56968 MW; E025D3124C8D6CE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 NQAKKMMQGVMSGDMNKVMKQMGINPNNMPNNMDSSALEGM 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 NDMKKNMKQFTGGGKGKKKRR-----NQMQN-----MLKGM 451
                                                                                                                                                                ; Pred. No. 1e-59;
82; Mismatches 115;
                                                                                                                                                     Score 1286;
Pfam, PF02978; SRP_SPB; 1.
ProDom; PD000819; SRP54; 1.
TIGREAMS, TIGRO0959; 3a0501s01; 1.
PROSITE; P800300; SRP54; 1.
                                                                                                                                                     56.68;
                                                                                                                                                                   Best Local Similarity 55.1
Matches 254; Conservative
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STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11528796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo B., Makayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Khara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterchemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampeli G., Satoh Y., Sivasuhaota S., Yamagata S., Horluchi T., Takeda J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Takemoto K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Johana K., Wada C., Yamagata S., Horluchi T., Takedo J., Takemoto K., Johana K., Wada C., Yamagata S., Horluchi T., Takedo J.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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Luirink J., High S., Wood H., Giner A., Tollervey D., Dobberstein B.;
"Signal-sequence recognition by an Escherichia coli ribonucleoprotein
SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MG1655;
MEDLINE-97426617; Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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MEDLINE-97053672; PubMed=8898086;
Oh D.-B., Yi G.-S., Chi S.-W., Kim H.;
"Structure of a methionine-rich segment of Escherichia coli Ffh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93063266; PubMed=1331806; Phillips G.J., Silhavy T.J.; Phillips c.oli ffh gene is necessary for viability and efficient protein export.";
                                                                                                                                                                                                                                                                                                                                                                                                            Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; Pubmed=11206551;
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ProDom; PD000819; SRP54; 1.
SAMRTY; SM0382; AAA; 1.
TIGRFAMS; TIGR00959; 3A0501801; 1.
PROSITE; PS00300; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILLER, ILLEGO, ILLEGO, ILLEGO, ILLEGO, ILLEGO, IPRO00897; SRP54.
INTERPRO; IPRO0125; SRP54_SPB.
INTERPRO; IPRO04780; SRP54_SPB.
Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54; 1.
Pfam; PF02891; SRP54; 1.
Probom; PD000819; SRP58; 1.
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                                                                                                                                                                                                                                                                       STANDARD;
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P44518;
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                       302
                                                                                                                                                                                                                                 RESULT 4
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                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                   -!- FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE
                                                                          SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 4.5 RNA MOLECULE AND PROTEIN FFH.

DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
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                                                                                                                                                                         SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
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                                                                                                                                                                                          CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 100.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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Signal recognition particle; GTP-binding; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                            EMEL, A010197; AAC756591; EMEL; BORBE, A010197; AAC756591; --
EMEL; D90889; BAA16495.1; ALT_FRAME.
EMEL; AB002491; AAC576591; ALT_FRAME.
EMEL; AP002562; BAB36896.1; --
PIR, S07178; S07178.
ECOGENE; S07178; S07178.
InterPro; IPR000897; SRP54.
InterPro; IPR000897; SRP54.
InterPro; IPR004185; SRP54.
InterPro; IPR004180; SRP54.
InterPro; IPR00819; IPR0081
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                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X01818; CAA25957.1; ALT_INIT.
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Lett. 395:160-164(1996).
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453
114
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251
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190
190
248
453 AA;
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                                                          RIBOSOMES
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STRAIN-E FROM N.B.

STRAIN-E STAGE N.B.

MEDIINE-95350630; PubMed=7542800;

MEDIINE-95350630; PubMed=7542800;

MEDIINE-95350630; PubMed=7542800;

MEDIINE-95350630; PubMed=7542800;

MELALAY & Madma M.D., White O., Clayton R.A., Kirkness E.F.,

MCKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

MCKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Wedoman J.F., Phillips C.A., Spriggs T., Hedblow E. Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;

Venter J.C.;

Venter J.C.;

Venter J.C.;

Venter J.C.;
362 DNVKSQMDDKVLVRMEAIINSMTMKERAKPEIIKGSRKRRIAAGCGMQVQDVNRLLKQFD 421
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-!- FUNCTION: NECESSARY FOR BFFICIENT EXPORT OF EXTRA-CYTOPLASMIC PROVETION: BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE RIBOSOMES (BY SIMILARITY).

-!- SUBUNIT: SIGNAL RECGNITION PARTICLE CONSISTS OF A 4.5 RNA MOLECULE AND PROTEIN FFH (BY SUMILARITY).

-!- DOMAIN: THE PROPEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
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                                                                                                                                       362 GLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQFN
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UNU-2002 (Rel. 41, Last annotation update)
Signal recognition particle protein (Fifty-four homolog).
FFH OR H10106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 AA
                                                                                                                                                                                                                                                                                                                                422 DMKKMMKQFTGGGKGKKGKRNQMQNMLKGMNLP 454
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DOMAIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 LYLRKQ-KRSALMVATDVYRPAAIDQLKTLGQQIDVPVFDLGSDANPVEIARQGVEKAKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 VTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 TLVEKAQEAIDVGDVEKLQNKILEATFDFDDFIKOMRFMKNMGSLGGLLKMIPGMNKLSS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: |::||: :||:||:||:||:||:||| FDALADFLEDAMKKLRGQDKISESNIKEALQEVRRALLAADVNLQVVKGFIKDVEQKALG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 FEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG 62
SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 4.5 RNA MOLECOLE AND PROTEIN FFH (BY SIMILARITY).

DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP: THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                          SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 462 M-DOMAIN.
107 114 GTP (BY SIMILARITY).
189 193 GTP (BY SIMILARITY).
247 250 GTP (BY SIMILARITY).
482 Aa, 52145 NW; F58B43596F9E66FI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal recognition particle; GTP-binding; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.4%; Score 1122.5; DB 1;
49.1%; Pred. No. 2.6e-51;
live 98; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDMKKMMKQF-TGGGKGKKGKRNQMQNMLKGM 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKMRTMMQQMGMGGMPGGMPGMGAMPGMGGGM 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004125; SRE54_SPB.
InterPro; IPR004780; SRE54_SPB.
Pfam; PF00448; SRE94; 1.
Pfam; PF02481; SRE94; 1.
Propon; PD00819; SRE54; 1.
SMART; SM00382; AAA; 1.
IIGREAMS; TIGR00959; 3a0501801; 1.
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003593; AAA_ATPase.
InterPro; IPR000897; SRP54.
                                                                                                                                                                                                                                                                                                                       EMBL; D90913; BAA18306.1; -. HSSP; 007347; 1FFH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00300; SRP54;
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                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim:
Matches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 VIGVTLIKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLIEKAQQDVDQEKAKDLEKKMRE-SSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKMK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 SLIEDLERSVDREKAEKMAQKFKKGDDFTLDDFREQLIEMKKMGGMMSMLEKLPGAKNLS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 GLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQFN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGKLA 122
                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                               3 FEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC PROFEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE RIBOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                     EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD
                                                                                                                                                                                            DB 1; Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal recognition particle protein (Fifty-four homolog). FFH OR SLR1531.
                                                                                    114 GTP (BY SIMILARITY).
194 GTP (BY SIMILARITY).
51 GTP (BY SIMILARITY).
50843 MW; 16AC32089A158F7A CRC64;
  GTP-binding; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Syneohocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                      50.0%; Score 1138; DB 1; Pred. No. 3.9e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 AA
                                                                                                                                                                                                                ; Pred. No. 3.9e
93; Mismatches
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                                              G-DOMAIN.
                                                                  M-DOMAIN.
    recognition particle;
                                                                                                                                                                                                                                       Conservative
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                                                            114
114
194
251
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248
262 AA;
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Signal recognition Complete proteome.
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Matches 225;
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TQVISGIRPDQQFIKVVYDBLVQVMGBTHVPLAQAAKAPTVILMAGLQGAGKTTATAKLA 121
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Packer J.C.L., Howe C.J.;
Plant MOL. Biol. 31:659-665(1996).
-!- FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC
PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE
RIBOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 4.5 RNA MOLECULE AND PROTEIN FRH (BY SIMILARITY).
-!- DOMAIN: THE PROPEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Packer J.C.L., Howe C.J.;
"The cyanobacterial genome contains a single copy of the ffh gene
encoding a homologue of the 54 kDa subunit of signal recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
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                                                                                                                                                                                                                                       Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 47.8%; Pred. No. 1.7e-50;
Matches 217; Conservative 100; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                789F3509127537AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal recognition particle; GTP-binding; RNA-binding. DOMAIN.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
                                                                    485 AA.
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HSSP; 007447; IFFH.
InterPro; IPR0000917; SRP54.
InterPro; IPR0004125; SRP54.
InterPro; IPR00448; SRP54.
Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54, 1.
Pfam; PF02881; SRP54, 1.
ProDom; PF000819; SRP54, 1.
PRODOM; PF000819; SRP54, 1.
PROSITE; PS000819; SRP54, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Mol. Biol. 30:659-665(1996).
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=96189278; PubMed=8605315;
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                                                                                                                                                                                       Signal sequence binding protein.
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193
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247 2
485, AA;
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01-NOV-1997 (
30-MAY-2000 (
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hirrisby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Ollver S., Osborner J., Quall M.A., Rajandream M.A., Rogers J., Ruter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the blology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                             302
                                                                                                                                                                                                                   362
                                                                                                                                                                                                                                          363 LDKLNMSEKQIDHIKAIIQSMTPAERNNPDTL--NVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                                                                                                                                                                            Bacteria, Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaeeae; Mycobacterium NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bishai W.\,; "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                          123 LLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKE
                    183 EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD
                                                                                                                                             243 VTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVL
                                                                                                                                                                                                                   SLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKMKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Signal recognition particle protein (Fifty-four homolog).
FFH OR RV2916C OR MT2984 OR MTCY338.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 421 QOMRIMMQQMSQGGFPGMG------GMGMP 444
                                                                                                                                                                                                                                                                                                                                                                 421 NDMKKMMKQFTGGGKGKKGKRNQMQNMLKGMNLP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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us-09-943-108a-2.rsp

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EMBL; AL583922; CAC30573.1; -. HSSP; 007347; 2FFH.
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Pfam; PF02481; SRP54, N; 1.
Pfam; PF02978; SRP SPB; 1.
ProDom; PD000819; SRP54, 1.
SWART; SM00812; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z97369; CAB10614.1; -.
                                                                                                                                                                                                    Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             521 AA;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                  NCBI_TaxID=1769;
                                             SR54_MYCLE
033013;
                                                                                                                                                                                                                                                                                                                                      STRAIN-TN;
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NP_BIND
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SEQUENCE
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                         SR54_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 LIMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYS-----EGDQVKPQQIVTN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 ARLRGQ-GHTPLLVACDLQRPAAVNQLQVVGERAGVPVFAPHPGASPESGPGDPVAVAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 ALKHAKEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFDDOLDVIGVILIKLDGDIRGGAALSIRSVIOKPIKFVGMSEKLDGLELFHPERMASRI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AFGEGVGFTGVALIKLDGDARGGAALSVREVTGVPILFASTGEKLEDFDVFHPDRMASRI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 LGMGDVLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 LGMGDVLSLIEQAEQVFDAQQAEEAAKIGAGELTLEDFLEQMLAVRKMGPIGNLLGMLP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 GMNKMKGLDKL-NMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 FEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 RIMKQFNDMKKMMKQFTG-------GGKGKKGKRNQMQNMLKGMNLP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 QLVERFFEARKMMSSMLGGMGIPGIGRKSATRKSKGAKGKSGKKSK-----KGTRGP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FESLSDRLTAAALQGLRGKGRLTDADIDATTREIRLALLEADVSLPVVRAFIHRIKERARG
                         SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36F6227BC367817C CRC64;
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M-DOMAIN (BY SIMILARITY).
GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDom; PD010819; SRP54; 1.
SMART; SM00382; AAA; 1.
TIGRRPAMS; TIGR00959; 3a0501s01; 1.
PROSITE; PS00300; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003593; AAA_ATPase.
InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004780; SRP54_SPB.
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525 M-
114 GT
200 GT
257 GT
55001 MW;
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EMBL; AE007120; AAK47310.1; -.
HSSP; O07347; 2FFH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00448; SRP54;
                                                                                                                                                                                                                                                                                                             TIGR; MT2984; -.
Tuberculist; Rv2916c;
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196
254
525 AA;
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Best Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1013(2001).
-!- FUNCTION: INCESSARY FOR BEFIGIENT EXPORT OF EXTRA-CYTOPLASMIC
-!- FUNCTION: NECESSARY FOR BEFIGIENT EXPORT OF EXTRA-CYTOPLASMIC
PROTEINS. BINDS TO FIRE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE
RIBOSOMES (BY SIMILARITY).
-!- SUBBNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A SWALL
-:- STUBNIT: SIGNAL RECOGNITION PARTICLE AND PROTEIN FFH (BY SIMILARITY).
-!- DOMAIN: THE PROFEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN
BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Hanibavis R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M., Squares S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.,
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                                                                                                                                                                                                                                                                                                    Bacteria, Actinobacteria; Actinobacteria (class); Actinobacteridae, Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE. SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
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                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Signal recognition particle protein (Fifty-four homolog).
FFH OR ML1622 OR MLCB250.20.
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GTP (BY SIMILARITY).
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521 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21128732; PubMed=11234002;
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InterPro; IPR003593; AAA_ATPase.
InterPro; IPR004947; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004180; SRP54_SPB.
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Best Local
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STRAINS-94012817; Pubmed=8408079;
Franklin A.E., Hoffman N.E.;
Characterization of a chloroplast homologue of the 54-kDa subunit of the signal recognition particle ", J. Biol. Chem. 268:22175-22180(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 564 AA.
P37107; 082570;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
11, Last annotation update)
11, Last annotation update, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Erassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                      412
                                                                           123 LIMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYS------EGDQVKPQQI 172
                                                                                                                                                              173 VINALKHAKEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVN 232
                                                                                                                                                                             238 TAAAFGAGVGFTGVVLTKLDGDARGGAALSVREVTGVPILFATTGEKLDDFDVFHPDRMA 297
                                                                                                                                                                                                                                                                  293 SRILGNGDVLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMK 352
                                                                                                                                                                                                                                                                                  63 SDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGKLA 122
                                                                                                                                       122 VRLRRQ-GHTPLLVACDLQRPAAVNQLQVVGERAGVPVFAPHPGASPDSGPGD---PVAV 177
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SEQUENCE FROM N.A.
STRAIN-CV. Columbia;
MEDLINE-21016721; PubMed-11130714;
Tabata S., Kaneko I., Nakamura Y., Kotani H., Kato T., Asamizu E.,
                      2 FESLSNRLTGVIQGLRGKGRLTDADIBATTRBIRLALFEADVSLPVVRAFVHRIKERARG
                                                                                                                                                                                                                                                                                                                                   |:|| ::| :: : :||:| ::|| || || :| || 358 MLPGAGQVKEVLE-QVDDRQLDRLQAIIRGWIPQERADPKIINASRRLKIANGSGVTVSE
                                                                                                                                                                                                                                                                                                                                                                                         3 FEGLSERLQATMQKWRGKGKLITEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG
                                                                                                                                                                                                                 233 VAESFDDQLDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMA
                                                                                                                                                                                                                                                                                                                     353 MIPGMNKMKGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQE
                                                                                                                                                                                                                                                                                                                                                                      413 VNRLMKQFNDMKKMMKQFTG-------GGKGKKGKKRNQMQNMLKG----
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Amin P., Sy D., Pilgrim M., Parry D.H., Hoffman N.E.;
Isolation of two Arabidopsis mutants in the nuclear gene ffc, encoding the 54 kDa subunit of chloroplast signal recognition particle.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
Rohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
RA Makazaki N., Matuo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Huange A., Yamada M., Sato S., de la Bastide M.,
Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
Stoncking T., Pepin K., Spieth J., Sakhon M., Armstrong J., Backer M.,
RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
RA DH H., Edwards J., Fryman J., Haakensen B., Lamar E., Iatreille P.,
RA Magner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
Ratichoff K., Toth K., Muson R.K., Murphy G., Bancroft I.,
RA Martienssen R., McCoulladh B., Robben J., Grymonprez B., Zinmermann W.,
RA Pansperger U., Wedler H., Balke K., Wedler E., Peters S.,
Langham S.-A., McCulladh B., Robben J., Grymonprez B., Zinmermann W.,
RA Ramsperger U., Wedler W., Mooijman P., Klein Lankhorst R.,
Ratzeneger T., Borthe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Ramsperger T., Borthe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Remsperger M., Mooijman P., Klein Lankhorst R.,
Reidpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
Reidbeller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.,
R., Hallen R., Balke K., Bevan M., Fransz P.,
R., Reidbeller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.,
R., Hallen R., Balke R., Robes B., Bevan M., Fransz P.,
R., Hallen R., Balke R., Robes B., Bevan M., Fransz P.,
R., Rober B., Rober B., Rober B., Bevan M., Fransz P.,
R., Rober B., Rober B., Rober B., Bevan M., Bevan R., Berneiser S., Hense R., Hellen R., Bevan M., Berneiser S., Hense R., Hellen R., Bevan M., Bevan M., Bevan R., Bevan R., Bevan R., Bevan R., Bevan R., R., Bevan R., Bevan R., Bevan R., R., Bevan R., R., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mountied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 408:823-826(2000).
-!- FUNCTION: MAY TARGET CHLOROPLAST PROTEINS TO EITHER THE THYLAKOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR ENVELOPE MEMBRANES.
--- SUBCELLULAR LOCATION: Chloroplast stroma.
--- TISSUE SPECIFICITY: WOST ABUNDANT IN GREEN SHOOT TISSUE AND LOWER LEVELS SEEN IN THE ROOTS AND ETIOLARED BUDS.
--- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
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E -> V (IN REF. 2).
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47.2%; Pred. No. 4.2e-46;
tive 96; Mismatches 130;
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EMBL; AR092165; AAC64139.1; --
EMBL; AL162873; CAB85514.1; --
FIR, S36637; S36637.
HSSP; 007347; IFFH.
InterPro; IPR000897; SRP54.
InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54.
Fam; PR0481; SRP54. 1.
Ffam; PR0281; SRP54. 1.
Ffam; PR0281; SRP54. 1.
Ffam; PR0281; SRP54. 1.
SMRT; SM00382; AAA, 1.
SMRRT; SM00382; AAA, 1.
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Matches 206; Conservative
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564
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                                                                                                        122
                                                                                                                                                                                                                                                                           SLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKMKG 362
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-!- DOMAIN: THE PROPEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GIP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                                                              Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
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                                                                                                        SDVMQSLTPGQQVIKIVQDELIKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGKLA
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30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Signal recognition particle protein (Fifty-four homolog).
FFH OR AQ_1720.
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Nature 39
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P57473; 09L4J1;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Signal recognition particle protein (Fifty-four homolog).

PRH OR BUSSA
Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon paymbiotic bacterium).

Bacteria; Proteobacteria; gamma subdivision; Buchnera.
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             InterPro; IPR003993; RAA_ATPase.
InterPro; IPR003997; SRP54.
InterPro; IPR004125; SRP54.
InterPro; IPR004125; SRP54.
InterPro; IPR00418; SRP54; 1.
Pfam; PP00448; SRP54; 1.
Pfam; PP00788; SRP54; 1.
Pfam; PP00798; SRP54; 1.
Pr0Dom; PD000819; SRP54; 1.
SWAFT; SW00382; AAA; 1.
ITGREAMS; ITGR00559; 3a0501801; 1.
PROSITE; SR00300; SRP54; 1.
Signal recognition particle; GTP-binding; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                        G-DOMAIN.
M-DOMAIN.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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102
182
184
242
454 AA;
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O07347; 1FFH
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242 ISGIILTKTDGDSRSGIALSMRYITGKPIKFIGTGEKIISLEPFHPERIADRILGMNDIM 301
                                                                                                                                                        SLIEKAQQDVDQEKAKDLEKKMRES-SFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM- 360
                                                                                                                                                                                                                                                361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
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DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP, THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Freymann D.M., Keenan R.J., Stroud R.M., Walter P., ^{\circ} "Structure of the conserved GTPase domain of the signal recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nat. Struct. Biol. 6:793-801(1999).
-!- FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC
PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE
                                                                                                                                                                                                    SLIEDIEEKVDQSQIQKLTKKLKKGHDFNLNDFLTQIKQMKKIGGLNYFANKFSINHQLS
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                                                                   VTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal recognition particle protein (Fifty-four homolog).
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Freymann D.M., Keenan R.J., Stroud R.M., Walter P.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=97155020; PubMed=9002524;
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16-OCT-2001 (Rel. 40, Last annotation update)
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DDIRRIMKKIKTDGIAKVIRGIKNML 447
                                                                                                                                                                                                                                                                                                                                   421 NDMKKMMKQFTGGGKGK--KGKRNQM 444
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15-JUL-1998 (Rel. 36, Last seq
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KWIKNKYKKKILITSTDTYRAAAIEQLKILSDQIEIDFFESDKHHTPIEITKNAIKYAKL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD 242
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                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBBNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 4.5 RNA MOLECULE AND PROTEIN FFH (BY SIMILARITY).
-!- DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GPP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                                                                                                                                                                                                                                          FIGURIAL NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE. SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                           Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                MEDLINE=20245558; PubMed=10781569;
Jimenez N., Gonzalez-Candelas F., Silva F.J.;
"Prephenate dehydratase from the aphid endosymbiont (Buchnera)
displays changes in the regulatory domain that suggest its
desensitization to inhibition by phenylalanine.";
J. Bacteriol. 182:2967-2969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 1; Length 451; 2.4e-45;
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

L -> I (IN REF. 1).

H -> N (IN REF. 1).

I -> T (IN REF. 1).

I -> L (IN REF. 1).

I -> L (IN REF. 1).

M; 6C6DF55FD9268A2C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 105; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.2%; Score 1006; 45.3%; Pred. No. 2.
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                                                                                                                                                                                                                    MEDLINE=20445173; PubMed=10993077;
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InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
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                                                                                                                                                                                                                                                                                                                                                                             RIBOSOMES (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal recognition particle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00448; SRP54; I. Pfam; PF02881; SRP54_N; 1. Pfam; PF02881; SRP54_N; 1. ProDom; PD000819; SRP54; 1. PROSITE; PS00300; SRP54; 1.
                                                                                                                                                                                                                                                                                                          Nature 407:81-86(2000).
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166
364
393
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451
114
194
251
                                                                                                                                 J. Bacteriol. 182:28
[2]
SEQUENCE FROM N.A.
STRAIN=TOKYO 1998;
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the European
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Matches 202;
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SEQUENCE FROM N.A.
                                                                           STRAIN=Madrid E;
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NP_BIND
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Best Local 9
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 SDVMQSLIPPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVVMAVGLQGAGKTTTAGKLA 122
                                                                                                                                                                                                                                                                                                                                                                    61 KQVLESLTPAEVILATVYEALKEALGGEARLPVLKDR--NLWFLVGLQGSGKTTTAAKLA 118
                                                                                                                                                                                                                                                                                                                                                                                      123 LIMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKE 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 SLAEKV-----RAAGLEAEAPKSAKELSLEDFLKOMONLKRLGPFSEILGILPGVPO- 349
                                                                                                                                                                                                                                                                                                                        21; Gaps
                                                                                                                                                                                                                                                                                                             3 FEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG 62
                                                                                                                                                                                     Signal recognition particle; GTP-binding; RNA-binding; 3D-structure. INIT_MET 0 0 G-DOMAIN.
                                                                                                                                                                                                                                                                         Length 429;
                                                                                                                                                                                                                                                                        44.2%; Score 1005.5; DB 1; Length 47.5%; Pred. No. 2.4e-45; Live 92; Mismatches 118; Indels
                                                                                                                                                                                                                                                     26D387A5A303EFBD CRC64;
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M-DOMAIN.
GTP (BY SIMILARITY).
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GTP (BY SIMILARITY).
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449 AA
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                                                                                                                                                           SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR00959; 3a0501s01; 1.
PROSITE; PS00300; SRP54; 1.
                                                                                Interpro; IPR003593; AAA_ATPase.
Interpro; IPR000897; SRP54.
Interpro; IPR004125; SRP54_SPB.
Interpro; IPR004780; SRP_sub.
                                                                                                                                                                                                                                                      47225 MW;
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                          EMBL, U82109; AAB58502.1; -
PDB; 1FFH; 31-DEC-97.
PDB; 2FFH; 16-U1L-99.
PDB; 1NGL; 13-WAR-00.
PDB; 3NGL; 13-WAR-00.
                                                                                                                      Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDom; PD000819; SRP54; 1.
                                                                                                                                                                                                                                                                                         Matches 209; Conservative
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                                                                                                                                                                                                                           111
190
247
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104
186
186
244
429 AA;
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Q9ZDZ0;
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NP_BIND
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SR54_RICPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINS, BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE RIBOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
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                                                                                                                                                                                                                                                                                         Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A. S., Winkler H.H., Kurland C.G., The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 FEGLSERLQATWQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 396:133-140(1998).
-!- FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 4.5 RNA MOLECULE AND PROTEIN FFH (BY SIMILARITY).
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                     FFH OR RP173.
Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
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ignal recognition particle protein (Fifty-four homolog).
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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Pred. No. 6.8e-43;
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                                                                                                                    Rickettsiaceae; Rickettsieae; Rickettsia
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TIGREAMS; TIGR00959; 3a0501s01; 1.
PROSITE; PS00300; SRP54; 1.
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InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004780; SRP_sub.
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Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDom; PD000819; SRP54; 1
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449 AA;
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us-09-943-108a-2.rsp

M-DOMAIN.

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DOMAIN
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NP_BIND
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                                                                                             357
                                                                                                                    358 NKM-KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRL 416
                                                                                                                                     SEKLEISGLILSRIDGDTKGGAALSVKYFTQKPIKFLSSGEKLTDLEBENAERLASRILD 297
            DDQLDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILG 297
                                                                 298 MGDVLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A Mycoplasma protein homologous to mammalian SRP54 recognizes a highly conserved domain of SRP RNR."; hulling conserved domain of SRP RNR."; hulling a solision of SRP RNR."; reduction in Becassary for Beprinteny Export of Extra-Cytoplasmic Proteins. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE RIBOSOMES (BI SIMILARITY).

-1- SUBMIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 4.5 RNA MOLECULE AND PROTEIN FPH (BY SIMILARITY).

-1- DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE; THE G-DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                  SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                      Signal recognition particle protein (Fifty-four homolog). FFH OR SRPM54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00300; SRP54; 1.
Signal recognition particle; GTP-binding; RNA-binding.
DOMAIN 1 295 G-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma mycoides.
Bacteria, Firmicutes; Mollicutes; Entomoplasmatales;
                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update
                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                           MKQFNDMKKMMKQFTGGGKGKKGKRNQMQNMLK 449
                                                                                                                                                                                                   418 LKOYKOISAVMK-----KTSKMNP-KNLLR 441
                                                                                                                                                                                                                                                                        447
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IIGRFAMS; TIGR00959; 3a0501s01; 1.
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InterPro; IPR003593; AAA_ATPase.
InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004780; SRP_sub.
Pfam; PF00448; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=93087189; PubMed=1280809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M91593; AAA25441.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
                                                                                                                                                                                                                                                                     STANDARD;
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PIR; S35481; S35481.
                                                                                                                                                                                                                                                                                                                                                                                              Entomoplasmataceae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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-!- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A SMALL CYTOPLASMIC RNA (SC-RNA) MOLECULE AND PROTEIN FFH (BY SIMILARITY).
-!- DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 33530 / G-37;
MEDLINE-96026346; PubMed-756993;
MEDLINE-96020346; PubMed-756993;
Fraser C.M., Googene J.D., White O., Adams M.D., Clayton R.A.,
Fraser C.M., Googene J.D., White O., Adams M.D., Clayton R.A.,
Frielschmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Petrson D.T., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Petrson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 VTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVLSLI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                              126 RKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKEEHL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 NKKNKKKVLLVGLDIYRPGAIEQLVQLGQKTNTQVFEKGKQ-DPVKTAEQALEYAKENNF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 MOSLTPGOQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGKLALLM 125
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                             6 LSERLQAIMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALGSDV 65
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                                                                                                                                                                                                                                                                                                                              186 DFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLDVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 VVVTKLDGDARGGATLSISYLTKLPIKFIGEGEGYNALAAFYPKRMADRLMGMGDIETLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 EKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKMKGLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 ERAVENIDERSIQKTMNRMFLGQFDLEDLRNQLAQIAKMGSLNKLMKNLP-INKVSE-SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 LNMSEKQIDHIKAIIQSMTPAERNNPDTLN-VSRKKRIAKGSGRSLQEVNRLMKQFNDMK
                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=2097;
                                                                                                                                                                      41.5%; Score 944; DB 1; Length 447; 44.2%; Pred. No. 3.8e-42; tive 93; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Signal recognition particle protein (Fifty-four homolog).
FFH OR MG048.
                                                                                                                         CRC64;
                              GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                      24A71128D4041D43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :: | | : | | : | | 423 KQVLEIT----KMIKSGRMPNLSKG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
447
115 GT
194 GT
251
50100 MW;
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Matches 197; Conservative
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   296
108
190
248
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P47294;
                                                                                                                      SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 AKEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 DVLSLIBKAQQDVDQBKAKDLEK---KWRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 MNKMKGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLN--VSRKKRIAKGSGRSLQEVN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 MQSLIPGQ----QVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGKL, 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LSSIVMRTWQKKINAQTITEKDVELVLKETRIALLDADVNLLVVKNFIKAIRDKTVG--- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALGSDV 65
BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                               -!- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.5%; Score 898; DB 1; Length 446; 43.0%; Pred. No. 8.8e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 43.0%; Fred. NO. 0.06-40;
Matches 198; Conservative 90; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 080F2255C8B5E5AE CRC64;
                                                                                                                                                                                                                                                                                                                                               TIGREAMS; TIGR00959; 3a0501s01; 1.
PROSITE; PR00300; SRP34; 1.
Signal recognition particle; GTP-binding; RNA-binding;
Complete proteome.
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Job time : 16 secs
                                                                                                                                                                                                                                                                                                                                                                                                                 G-DOMAIN.
M-DOMAIN.
                                                                                                                                                                                                                                    InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004780; SRP_sub.
Pfam; PF00448; SRP54, 1.
Pfam; PF02881; SRP54_N, 1.
Pfam; PF02891; SRP54_N, 1.
Probom; PD000819; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50199 MW;
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HSSP; O07347; IFFH.
TIGR; MG048; -.
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446
113
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446 AA;
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NP_BIND
SEQUENCE
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09CLN6 09CLN6 09JK177 09JKK2 09JKK2 06RVK2 08KVM3 08ST74 08ST74 08ST74 08ST76 09RC0 09RC0 09RC0 09RC0 09RC1 09RUC0

1135.5 11131 11130 11130 11130 11123 11092.5 10092.5 10092.5 10092.5 10092.5 10092.5 10092.5 10092.5 10093.5 993.5 993.5 993.6 8698 8688 8688 8468

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February 21, 2003, 15:15:12; Search time 35 Seconds (without alignments) 2678.612 Million cell updates/sec
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2274
1 MAFEGLSERLQATMQKMRGK......GKKGKRNQMQNMLKGMNLPF 455
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            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                               OM protein - protein search, using sw model
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2: sp_bacteria:*
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7: sp_nhc:*
8: sp_organelle:*
9: sp_pand:*
10: sp_plant:*
11: sp_rodent:*
11: sp_rodent:*
12: sp_virue:*
13: sp_vertebrate:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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ALIGNMENTS

Q9PL14 O84028 Q9JRV9 Q9Z966

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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099un3 staphylococ 08y695 listeria mo 092a7 listeria in 092a7 listeria in 097198 clostridium 08xp3 clostridium 08xp3 chermoanaer 09cf65 lactococcus 099x1 streptococc 099x1 fusobacteri Description 2990N3 281695 292AK7 29KA10 297198 28RAJP3 28RAJP3 28CAJP3 Query Match Length DB 2274 1717.5 1717.5 1708.5 1388.5 1352.6 1352.5 1315.5 1279.5 1180.5 1150.5 1150.5 Score

thermotoga salmonella vibrio chol pseudomonas yersinia pe

O9x1q1 O8xf48 O9kug1 O9hxp8 O8zbu6

09X1Q1 08XF48 09KUG1 09HXP8

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LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAFEGLAGRLQETMNKIRGKGKVNEADVKEMMREVRLALLEADVNFKVVKQFIKTVSERA 60
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Bagnero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann B., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 450;
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                                                                                                                                                                                                                                                                                                                       450 AA; 49714 MW; D5888D7A99C60C76 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                   75.5%; Score 1717.5; 72.7%; Pred. No. 3.2e
                                                                                                                                                                                                                                                                                                                                                                                                                  64; Mismatches
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TIGRFAMS; TIGR00959; 3a0501s01; 1.
                                     ListiList; IMO01801; -.
InterPro; IPR003593; AAA_ATPase.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CLIP 11362 / SEROVAR GA;
PubMed=11679669;
                                                                               InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004780; SRP_sub.
         EMBL; AL591981; CAC99879.1; -.
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                                                                                                                                                 Pfam; PF00448; SRP54; I. Pfam; PF02881; SRP54_N; I. Pfam; PF02978; SRP_SPB; I. ProDom; PD000819; SRP54; I.
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 331; Conservative
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NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes;
                                     ListiList; LMO01801
                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 450 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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FFH OR LIN1915.
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A Glaser P., Frangel L., Buchrieser C., Rusnick C., Amend A.,
A Charbit A., Chercumani F., Couve E., de Daruvar A., Dehoux P.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
A Jones L.-M., Kaerst U., Kreft J., Kuhn T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Matcurnam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ 240
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                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                             1 MAFEGLSERLQATMOKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                        0;
                                                                                                                                                    DB 16; Length 455;
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Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
NCBL_TaxID=1639;
                                                                                                                                                                                                   Indels
                                                                                                     619A202B1734097C CRC64;
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Last annotation update)
                                                                                                                                            100.0%; Score 2274; DB 16;
100.0%; Pred. No. 6.2e-114;
ive 0; Mismatches 0;
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SEQUENCE FROM N.A.
STRAIN-EGD-E / SEROVAR 1/2A;
MEDLINE-21537279; Pubmed-11679669;
SMARI; SM00382; AAA; 1.
TIGREAMS: TIGR00959; 3a0501s01; 1.
                                                                                                455 AA; 50753 MW;
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                           TIGRFAMS; TIGR00959; 3a0501
PROSITE; PS00300; SRP54; 1.
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Matches 455; Conservative
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                                                                     Complete proteome. SEQUENCE 455 AA:
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FFH OR LMO1801.
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LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMAVGLQGAGKTTTAGK 120
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                                                                                                                                                                  Horikoshi K.;

"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.";

"Nucleic Acids Res. 28:4317-4331(2000).

EMBE; AP001515; BAB06203.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAFESLABRIQDTLKKIRGKGKVSEQDVKEMMREVRLALLEADVNFKVVKQFIANVKEKA 60
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Clostridium acetobutylicum.
Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridia;
             SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE-20512582; Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., M. Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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01-007-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Signal recognition particle GTPase Ffh.
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TIGRFAMS; TIGR00959; 3a0501s01; 1.
PROSITE; PS00300; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR003593; AAA_ATPase.
Interpro; IPR001897; SRP54.
Interpro; IPR004125; SRP54_SPB.
Interpro; IPR004780; SRP_sub.
Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54, 1.
Pfam; PF02981; SRP54; 1.
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Matches 307; Conservative
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Q97198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||| : : :||: ||:|||:||| ||::||| :||||:||||:||||:||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kureft J., Kunh M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., NG E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P., Comparative genomics of Listeria species."; Comparative Garcial Section 294:649-682(2001).

Examb., ALS96170; CAC97145.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 450;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.1%; Score 1708.5; DB 16; Lengtl Best Local Similarity 72.3%; Pred. No. 9.7e-84; Matches 329; Conservative 65; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 AA; 49684 MW; E417626D1D69D239 CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-0UN-2002 (TrEMBLrel. 21, Last annotation update)
Signal recognition particle.
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Pfam; PF02881; SRF54_N; 1.
Pfam; PF02978; SRF54_N; 1.
ProDom; PD000819; SRF54; 1.
TIGRFAMS; TIGR00959; 3a0501801; 1.
                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004780; SRP_sub.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=86665;
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Q9KA10

RESULT 4 Q9KA10

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121 LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
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                                                                                                                                                                                                                                                                                                        Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.8%; Score 1382; DB 16; Length 452; 62.7%; Pred. No. 2.7e-66; 1ve. 72; Mismatches 86; Indels 8
                                                                                      Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
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SEQUENCE 452 AA; 49685 MW; 2356112EDC9C7D31 CRC64;
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

EMBL, AP003191; BAB81419.1; -

InterPro; IPR003993, AAA_ATPASe.

InterPro; IPR000897; SRP54_SPB.

InterPro; IPR004125; SRP54_SPB.

InterPro; IPR004786; SRP54, I.

Pfam; PF00248; SRP54, I.

Pfam; PF002881; SRP54_N; I.

ProDom; PD000819; SRP54, I.
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                                Signal recognition particle protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00300; SRP54; UNKNOWN_1.
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TIGRFAMS; TIGR00959; 3a0501s01; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 62.7%
Matches 279; Conservative
                                                                                                                                                                                                                                                                     TYPE A;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     STRAIN=13 / TYPE PubMed=11792842;
                                                                                                                                                                            NCBI_TaxID=1502;
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Q8R9X0
ID Q8R9X
AC Q8R9X
DT 01-JU
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AMELINE-21353325; PubMed-1186286;

AMELINE-21353325; PubMed-1186286;

AMELINE-21353325; PubMed-11466286;

AMELINE-21353325; PubMed-11466286;

AGISSON R., Lee H.M., DubOls J., Mitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing

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"Tenome sequence analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.3%; Score 1393; DB 16; Length 449; 61.0%; Pred. No. 6.9e-67; Live 71; Mismatches 94; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 AA; 49555 MW; FF4695E75A673733 CRC64;
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TIGREAMS; TIGR00959; 3a0501s01; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS00300; SRP54; UNKNOWN_1.
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Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                   STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 280;
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Best Local S
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Q8XJP3;
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RESULT 6 Q8XJP3

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MEDLINE-21235186; PubMed=11337471; Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus "The complete genome sequence of the lactic acid bacterium Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMYGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 LDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
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Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaceae; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.8%; Score 1315; DB 16; Length 518; 55.4%; Pred. No. 1.2e-62; live 88; Mismatches 102; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N------DMKKMMKQFTGGGKGKKGKRNQMQNMLKGMNLP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518 AA; 56845 MW; BF4539EF037601B4 CRC64;
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Last sequence update)
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01-0CT-2001 (TrEMBLrel. 18, Last seq
01-UN-2002 (TrEMBLrel. 21, Last ann
Signal recognition particle protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR00959; 3a0501s01; 1.
PROSITE; PS00300; SRP54; UNKNOWN_1.
                                                                                                                                                                                                                     | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | Dieter | D
                                                                                                                                lactis ssp. lactis IL1403.";
Genome Res. II:731-753(2001).
EMBL, AE006591; AAK05714.1; --
HSSP; 007347; IFFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.44
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Q97QD2
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                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVYDSMTGQDAVNVAESFDDQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 LGQEVMESLTPAQQVIKIVHEELIKLMGSVESRINLGSKVPAVIMAVGLQGSGKTTACGK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 MAFESLSERLÖGVFKKIRGKGKLTEKDIKEAMREVKVALLEADVNFKVVKDFINSVTEKA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                            STRAIN-MB4T / JCM11007;
MEDLINE-21992816; PubMed=11997336;
MEDLINE-21992816; PubMed=11997336;
Dao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xu Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
R. Complete sequence of T. tengcongensis genome. ";
Genome Res. 12:689-700(2002).
EMBL; AE013104; AAM24684.1; -.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
59.5%; Score 1352.5; DB 16; Length 447;
Best Local Similarity 59.9%; Pred. No. 1e-64;
Matches 273; Conservative 74; Mismatches 96; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 AA; 49294 MW; 3DB00C468FA14B7E CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Signal recognition particle GTPase.
Fig. 0R TIE1462.
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Last annotation update)
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EETKKMMKRFADIDKDLKRGK------LRLPF 445
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                                                                                                 Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes; Bacillus/Clostridium
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01-JUN-2001 (TrEMBLrel. 17, Last sequenco
01-JUN-2002 (TrEMBLrel. 21, Last annotat
Signal recognition particle protein Ffh.
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                                                                                                                                                                           NCBI_TaxID=119072;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Q9CF65
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Streptococcaceae; Streptococcus.
NCBI_TaxID=1314;
                                                 Streptococcus pyogenes.
                                                                                                         SEQUENCE FROM N.A.
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Q8RDV7
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                                          Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Peldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Dougherty B.A., Morrison D.A., Pallingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LALIMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                          523 AA; 57757 MW; A31745B7898470F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        91; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 NDMKKMMKQFTGGGKGKKGKRNQMQNMLKGM----NLP 454
                                                                                                                                                                                                                                                                                                                                                                 57.4%; Score 1306; DB 16
54.9%; Pred. No. 3.7e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         099ZK1;
01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGRO0559; 3a0501s01; 1. PROSITE; PS00300; SRP54; UNKNOWN_1 Complete proteome. SEQUENCE 523 AA; 57757 MW: A317
                                                                                                                                                                                             InterPro; IRR003593; AAA_Arpase.
InterPro; IPR000897; SRP54.
InterPro; IRR004125; SRP54_SPB.
InterPro; IRR004780; SRP54_SPB.
Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54; 1.
Pfam; PF02881; SRP54; 1.
Probom; PF02989; SRP589; 1.
                      STRAIN=TIGR4;
MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                             Science 293:498-506(2001).
EMBL; AE007428; AAK75391.1; -.
TIGR; SP1287; -.
                                                                                                                                                                                                                                                                                                                                                                                        Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                    pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q992K1
                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
Q99ZK1
ID Q99ZK:
AC Q99ZK:
DI 01-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Olan Y., Jia H.G., Najar E., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an MI strain of Streptococcus pyogenes.", Proc Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBI, AE006560; AAK34060.1; -. 98:4658-4663(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.3%; Score 1279.5; DB 16; Lengt Best Local Similarity 54.9%; Pred. No. 9.6e-61; Matches 251; Conservative 86; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 AA; 57415 MW; EF1E46696A1C0040 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Putative signal recognition particle. FFH OR SPY1200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 NDMKKMMKQFTGGGKGKKGK-----RNQMQNMLKGM 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 NQAKSMMQGVMSGDMSKMMKDMGINPNNLPKNMPAGM 456
                                                                                                                                                                                                                                                                                                                      STRAIN-SF370 / ATCC 700294 / SEROTYPE MI;
MEDLINE-21192684; PubMed=11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00300; SRP54; UNKNOWN_1.
Complete protecome.
SEQUENCE 519 AA, 57415 MW: FF1FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003593; AAA_Arpase.
InterPro; IPR000897; SRP54.
InterPro; IPR0004125; SRP54_SPB.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR00448; SRP94; 1.
Pfam; PF00848; SRP94; 1.
Pfam; PF02978; SRP-54_N; 1.
ProDom; PD000119; SRP54; 1.
SWART; SW00382; AAA; 1.
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Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., Mite O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGKLA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 EEVLRSLTPDOOPIKIVRDELVRIMGEKNEPLRLVHR-PAPIMMVGLOGSGKTTTCAKLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 LIMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 VTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKMKG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 LDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQPND 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 FEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.9%; Score 1180.5; DB 16; Length 433; 53.4%; Pred. No. 1.5e-55; Live 92; Mismatches 99; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteome.
433 AA; 48701 MW; B907E982F4D29357 CRC64;
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TIGRFAMS; TIGR00959; 3a0501s01; 1.
PROSITE; PS00300; SRP54; UNKNOWN_1.
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                                                SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed=10360571;
                                                                                                                                                                                                                                                                                             InterPro; IPR003593; AAA_ATPase.
InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004780; SRR_Sub.
                                                                                                                                                                                                                           Nature 399:323-329(1999).
EMBL, AE001802, AAD36632.1, -.
HSSP, 007347, 1FFH.
TIGR, TM1565, -.
                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00448; SRP54; 1.
Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP SPB; 1.
ProDom; PD000819; SRP54; 1.
SMART; SM00382; AAA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 MKALMKRM-----KKGR 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                    NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query, Match
Best Local (
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Q8XF48;
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ID Q8
AC Q8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 IMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKEE 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 TGVTLIKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVLS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 LIEKAQQDVDQEKAKDLEKKMRESSFILDDFLEQLDQVKNLGPLDDIMKMIPGMNKMKGL 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Barthan A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walumas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain Arcc 25586.";
J. Bacteriol. 184:2005-2018(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 EGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALGS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ENLGNRRQDIFKKIRGHGKLSETNIKDALREVKMSLLEADVNYKVVKDFTNRISEKAIGT 62
                                                                                                                                                                                                                                                                                                                                                                                                                         54.4%; Score 1238; DB 16; Length 444; 54.2%; Pred. No. 1.3e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          86; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                           444 AA; 48966 MW; F2593E0D3F0F851A CRC64;
                              (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                               Signal recognition particle, subunit FFH/SRP54
 444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 AA
                                                                                                               Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
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 PRT;
                                                                                                                                                                                                            MEDLINE=21886394; PubMed=11889109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 245; Conservative
PRELIMINARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                   ll,
SEQUENCE FROM N.A.
STRAIN=ATCC 25586;
                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
                                                                                                                                             NCBI_TaxID=76856;
                                01-JUN-2002
                                             01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                O8RDV7;
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Q9X1Q1
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183 EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSWTGQDAVNVAESFDDQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR000897; SRP54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel, 21, Last and Signal recognition particle protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004125; SRP54_SPB. InterPro; IPR004780; SRP_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE004142; AAF93728.1; -. HSSP; 007347; IFFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54, N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDcom; PD000819; SRP54; 1.
SMART; SM00382; AAA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIGR; VC0560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9KUG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                               SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; MEDLINE=21534948; PubMed=11677609; MCClelland M. P. Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Uturcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Daviss R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Woule S., O'Gaora P., Parry C., Quall M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDVMQSLTPPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGKLA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 HEVNKSLTPGOEFVKIVRSELVAAMGEENQTLNLAAQPPAVVLMAGLQGAGKTTSVGKLG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEGLSERLQATMOKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: 1::11 |:::: |::|| |::::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi\ CT18.";
                                                                                                                                                                                                                Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; DB 16; Length 453;
7e-55;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0JN-2002 (TrEMBLrel. 21, Last annotation update)
4.5S-RNP protein, GTP binding export factor, part of signal recognition particle with 4.5 RNA (Signal recognition particle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF0F70616A2111BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
PROSITE; PS00300; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1173.5;
Pred. No. 3.7e-
93; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00359; AAA_APPase.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR004915; SRP54_SPB.
InterPro; IPR0041780; SRP54_SPB.
InterPro; IPR004488; SRP54_N1.
Pfam; PR00448; SRP54_N1.
Pfam; PR02978; SRP54_N1.
ProDom; PR000819; SRP54_N1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-S.typhi; STRAIN-CT18;
MEDLINE-21534947; PubMed-11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00382; AAA; 1.
TIGREAMS; TIGR00959; 3a0501s01; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:848-852(2001).
EMBL; AE008821; AAL21566.1; -.
EMBL; AL627276; CAD05856.1; -.
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51.4%;
                                                                                                                                                               Salmonella typhimurium, and Salmonella typhi.
                                                                                                                                         FFH OR STM2677 OR STY2864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413:852-856(2001).
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                                                                                                                                                                                                                                      Salmonella.
NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 233; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 453 AA;
                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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MEDLINE-20406833; PubMed=10952301;
MEDLINE-20406833; PubMed=10952301;
Meidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelln H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
242
                                                        241
                                                                                                                                                                                                                                    361
                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                                                                                        362 GLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQFN 421
                                                                                                                                                                                                                                                                                                                                                                                                                   362 DNVKSQMDDKVLVRMEALINSMTLKERAKPEIIKGSRKRRIAQGCGMQVQDVMRLLKQFD 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                            242 LIGVVLTKVDGDARGGAALSIRHITGKPIKFLGVGEKTDALEPFHPDRIASRILGMGDVL
                                                                                                                                                                                                                                       SLIEKAQQDVDQEKAKDLEKKMRE-SSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKMK
                                                                                                                                                                                                                                                                       243 VTGVILTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 FEGLSERLQATMQKWRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616E9291972B3CDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
PROSITE; PS00300; SRP54; 1.
COMDIÈTE PYCLEOME.
COMDIÈTE 461 AA; 50373 WW; 616E9291972B3CDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.6%; Score 1150.5; DB 50.8%; Pred. No. 6.4e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMKKMMKQFTGGGKGKKGKRNQMQNMLKGMNLP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMQRMMK-----KMKKGGMAKMMRSMKGMMPP 448
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STRAIN=ANCC 15692 / PAO1;
STRAIN=ANCC 15692 / PAO1;
STRAIN=ANCC 15692 / PAO1;
STRAIN=ANCC 15692 / PAO1;
StORE C.K., Phan X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Mestbrock-Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 SDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGKLA 122
                   183 EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD 242
                                                                                                                                             243 VIGUTLIKLDGDIRGGAALSIRSVIQKPIKFVGMSEKLDGLELFHPERMASRILGMGDVL 302
                                                                                                                                                                                                           303 SLIEKAQQDVDQEKAKDLEKKMRE-SSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKMK 361
                                                                                                                                                                                                                                                                             |||| ||:||||||: ||||:|| 302 SLIEDLQRNVDQEKAEKLAKKFKEKKGFDLEDFREQLGQMKNMGGMMGMLDKLPGMSQLP 361
                                                                                                                                                                                                                                                                                                                    362 GLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQFN 421
                                                                                                                                                                                                                                                                                                                                           LLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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TIGRRAMS; TIGRRAMS; TIGRRAMS; TIGRRAMS; TIGROUSS9; 3a0501801; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
PROSITE; PS00300; SRP54; 1.
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InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004780; SRP_sub.
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01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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Nature 406:599-964 (2000).
EMBL; AE004793; AsdG7133.1; -.
HSSP; C07347; 1FFH.
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SEQUENCE 457 AA; 49359 MW;
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Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDom; PD000819; SRP54; 1.
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50.6%; Score 1150; DB 16; Length 457; 50.5%; Pred. No. 6.7e-54; tive 93; Mismatches 121; Indels 12;
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Job time : 42 secs

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-UOSER-US09943108_CGGN_1_1_2874_@runat_21022003_151631_1824 -NCDU-6 - ICPU-3
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Mismatches:
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High quality sequence start: 30
High quality sequence stop: 2141.
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                                                                                                                                                              Email: sorokine@jouy.inra.fr
best homologue in strain IL1403
(2002) In press
                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .2169
                                                                                                                                                                                                                                                                                                                                                  /strain="MG1363"
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73.86%
55.33%
47.23%
                                                                                                                Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
                                                Genetique Microbienne
                     Contact: Sorokin A
  Sci. Aliments,
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/note="Vector: Lambda DASH II; sequenced using Li-Cor
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Salmonella.
1 (bases 1 to 875)
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AF075878 Salmonella typhimurium LT2, Lambda DASH II Salmonella
typhimurium genomic clone 245-T3, DNA sequence.
AF075878
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294
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GlyMetSerGluLysLeuAspGlyLeuGluLeuPheHisProGluArgMetAlaSerArg
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Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego,
Email: mcclelland@lifsci.sdsu.edu
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/db_xref="taxon:602"
/clone="245-T3"
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us-09-943-108a-2.rst

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primer: T3
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Best Local Similarity:
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773 bp mRNA linear EST 18-OCT-2001 SST554007 tomato flower, anthesis Lycopersicon esculentum cDNA B1934118 GI:16248590
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids 1; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
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van der Hoeven, R. S., Bezzerides, J. L., Karamycheva, S. A., Tsai, J.,
Utterback, T., Van Aken, S., Ronning, C. M., Nierman, W., Fraser, C. M.,
Martin, G. B., Giovannoni, J. J. and Tanksley, S. D.
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
First clone is available through the Clemson University Genomics
Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeupheGlualaAspvalAsnPheLysvalValLysGluPheIleLysThrvalSerGlu
||| |||||||||||||||
|CTTTPAGAAGCTGATGTTCCCAGTTGTCAGAAGGTTTGTTCAGTCTAGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgAlaLeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIle
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134
60
63
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="tomato flower, anthesis"
/tissue_type="flower"
/dev_stage="anthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOD18J16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.83e-69
715.50
75.198
51.948
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δ QQ δŽ g  $\delta$  g QΫ g  $\Omega$ 셤 ä g ð g  $Q_{\overline{Q}}$ g δλ g

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/lab_host="B. coll SOLK"

/note="Vector: Lambda ZAP II, excised phagemid; Site_I:
BCORI; Plants were grown under six following different
environmental regimes in greenhouse. Environment 1)
240c/170c day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 240c/170c day/night,
well-watered, without post-anthesis fertilizer,
Environment 3) 370c/170c day/night, well-watered, without post-anthesis fertilizer,
Environment 3) 370c/170c day/night with
post-anthesis fertilizer, Environment 4) 370c/170c
day/night, well-watered, without post-anthesis fertilizer,
Environment 5) 370c/170c day/night plus drought, with
post-anthesis fertilizer, Environment 6) 370c/170c
day/night plus drought, without post-anthesis fertilizer,
developing wheat grains from the following were excised
and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,
8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 pps. Environment
2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44
DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 31 dpps Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by 8.
Altenbach and K. Cronin at USDA-ARS, Albany, CA. A CDNA
library was made using poly (A) RNA, and the CDNA clones
were in vivo excised to give pluescript SK1, phagemids
in the TJ Close lab (Chin, Close, Fenton) at the
University of California, Riverside. Placamid DNA
preparations and DNA sequencing were performed in the DDA
Anderson lab (Chins, Electron Parkerson in the PDDA
Anderson lab (Chins) and PNA sequencing were performed in the DDA
Anderson lab (Chins, Electron Parkerson in the PDDA
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 TyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIleProVal 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 TyrserGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLysHisAla 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysGluGluHisLeuAspPheValIlelleAspThrAlaGlyArgLeuHisIleAspGlu 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeu 280
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     /tissue_type="whole grains"
/dev_stage="3-44 days post anthesis seed"
/lab_host="E. coli Solr"
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116
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115 c 179 g
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75.23%
53.21%
27.75%
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Best Local Similarity:
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Contact: Olin Anderson
Contact: Olin Anderson
West Area, Western Regional Research Center
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Littucata, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Enbryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum. | (bases 1 to 656) | Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin, K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 31-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The structure and function of the expressed portion of the wheat genomes - Developing grains CDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ805434 15.2242S Wheat developing grains cDNA library Triticum aestivum cDNA clone WHE3566_H12_P24, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                      239 AspGlnLeuAspValThrGlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGly 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GlyLysLeuAlaLeuLeuMetArgLysLysTyrAsnLysLysProMetLeuValAlaAla 138
                                  179 HisAlaLysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIle 198
                                                                                                                                                                                                                                                                                                                                                                    418 GAGGCCAAAAAGAAGAAGAATGTAGTAGTCATAATGGATACAGCTGGAAGACTTCAGATA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 MetLeuValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAsp 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCGAAATTGGGATTACTGGTGCCATCTTGACGAAGCTAGATGGAGATTCTAGGGGTGGA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 AlaAlaLeuSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGlu 278
                                                                                                            AspileTyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspile 158
                                                                                                                                                                                                                      159 ProValTyrSerGluGlyAspGlnValLysProGlnGlnIleValThrAsnAlaLeuLys 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Triticum aestivum"
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/db_xref="taxno" 145_8"
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/clone_lib="Wheat developing grains cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 LysLeuAspGlyLeuGluLeuPheHisProGluArgMetAlaSerArgIleLeu 296
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Fax: 5105595818
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HTC 19-JAN-2002
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AR011928
AR011928 I GI:12848353
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:561029G12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                       GATATTGAAGTATTCCATCCAGATAGAATGGCTTCAAGAATATTAGGAATGGGAGAGTGT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 TIGAAGGCAITGAT---TITICICAAGGAGAAAAACAAATGGCIACAGITAAAGCAAICA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 TACAATCGATGACAGCTAAAGAAAGAAAACAACCTTCTTTAGTAATAGGAAATGGTTCAA 112
                                                                                                   301 lLeuSerLeulleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeuGl 321
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                                                                                                                                                           ValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeu 241
                                                                                                                                                                                                                                                                                                                    261 uSerIleArgSerValThrGlnLysProIleLysPheValGlyMetSerGluLysLeuAs 281
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                                                                                                                                                                                 AspValThr-GlyValThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAlaLe
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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  Gaps:
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Tissue Procurement: Dr. James Lupski
CDNA Library Preparation: Lupski Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                    BF940797 111 bp mRNA linear EST 22-JAN-2001 7d99a06.xl Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3280811 3' similar to SN:SR54_BACSU P37105 SIGNAL RECOGNITION PARTICLE PROTEIN ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5'-GACTAGTTCTAGATCGCGAGCGCCCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 711) MCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                           320
                                                                                                                                      GluLysLysMetArgGluSerSerPheThrLeuAspAspPheLeuGluGlnLeuAspGln 340
                  GAGGACCTTGAGCTTTTCTATCCCGACCGCATGGCACAACGTGTTTTGGGAATGGGAGAT 482
                                                                                                 GICCITICALITIGITGAAAAAGCACAAGAAGTCGTTCGCCAAGAGGATACCATGGAACTG 542
                                                                                                                                                                             543 CAGAAGAAGAICAIGAGIGCGAAAITIGACITCAAFGACITITTTAAAGCAGACACAAAAI 602
                                                         ValLeuSerLeuIleGluLysAlaGlnGlnAspValAspGlnGluLysAlaLysAspLeu
341 VallysAsnLeuGlyProLeuAspAspIleMetLysMetIleProGlyMetAsn 358
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/sex="male"
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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Length:
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/db_xref="taxon:9606"
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Seg primer: -40UP from Gibco
High quality sequence stop: 433.
Location/Qualifiers
1.711
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VIMFVGLQGSGKTTTCSKLAYYYQRKGWKTCLICADTFRACAFDQLKQNATKARIPFY
GSYTEMDPVIIASEGVEKFKNENFEIIIVDTSGRHKQEDSLFEEMLQVSNAIQPDNIV
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BHIDDFEPFRYQPFISKLLGMODIEGLIDKVNABLLIBKLHAGHTIKKKHOGFTLRDMYE
OFQNITMKMGPF3GILGWIFGFGTDFWGKRDGESKARLKLATINGSMUDGELDSTDG
AKVFSKQPGRIQRVARGSGVSTRDVQELLIQYTKFAQMVKKMGGIKGLFKGEDMSKNV
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/clone_lib="RikEN full-length enriched mouse cDNA library"
/dev_stage="10 days embryo"
1. .2387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="MGD:MGI:1346087"
/translation="MVLADLGRKITSALRSLSNATIINEEVLNAMLKEVCTALLEADV
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                               /db_xref="FANTOM_DB:2610209C12"
/db_xref="MGD:MGI:1905318"
/db_xref="taxon:10090"
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/db_xref="GI:12848354"
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                 Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374
                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, T., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikwar, T., Ozawa, K., Tanaka, T., Matsunira, S., Kawai, J., Karaki, Y., Miramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B. J. Direct Submission of BAC-end sequences from Anopheles gambiae
                                                                                                                                                                                                                                                                                            This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas AAM University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 IleTyrArgProAlaAlaIleAsnGlnLeuGlnThrValGlyLysGlnIleAspIlePro 159
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                    Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 AlaLeuGlySerAspValMetGlnSerLeuThrProGlyGlnGlnValIleLysIleVal
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Conservative:
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Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .688 /
/organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="PEST"
/db.xref="taxon:7165"
/clone="xdG-ND-138B11"
/clone=11b="ND-TAM"
/note="Vector: pECBAC1; 53
a 118 c 154 g 193
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   Anopheles gambiae
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Best Local Similarity:
Query Match:
                    Sukaryota;
                                                           Anopheles.
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                                                                      181 LysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHisIleAspGlu 200
                                                                                           ValValAspSerMetThrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGln 240
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                                    715 TATGGCAGCTATACTGAAATGGATCCTGTCATCATTGCTTCTGAAGGAGTGGAGAAATTC 774
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Query Match: 24.74% Indels: 1 DB: 10 Gaps: 1	-09-943-108A-2 (1-455) x BE432304 (1-605) 65 ValMetGlnSerLeuThrProGlyGlnGlnValIleLyslleValGlnAspGluLeuThr .::::::::::::::::::::::::::::::::::::	DD 2 TYCATICGAGGIGTAAAACCAGATCAGGTAAGACIGTACGTACGAGGACGAGGGTIGTG 51 QY 85 LysLeuMetGlyGlyGluAsnThrSerIleAsnMetSerAsnLysProProThrValVal 104	OY 105 MetMetValGlyLeuGlnGlyAlaGlyLysThrThrAlaGlyLysLeuAlaLeuLeu 124 ::::::	Oy 125 MetarglyslystyrasnlyslysProMetLeuValalaalaaspileTyrArgFroala 144 :::	:::	DD 259 ACAGATGIAMARICCIGCAGAAATAGCCCGGACATACAAGAGGCCCAAAAAAGAGI 550  QY 185 LeuaspPheVallleileaspPhralaGlyArgLeuHisIleaspGlualaLeuMetasn 204  :::	QY 205 GluLeuLysGluValLysGluIleAlaLysProAsnGluIleMetLeuValValAspSer 224	225 WetthrGlyGlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeuAspValThr 	Oy 245 GlyvalThrLeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAlaLeuSerIleArg 264	Qy 265 Serval 266     Db 599 GAGGTA 604	AM648731 AW648731 LOCUS LOCUS DEFINITION BEST327101 tomato germinating seedlings, TAMU Lycopersicon Associating and Alone AFFFG22 5, mpNA seculence	ACCESSION AW648731 VERSION AW648731.1 G1:7409885 KEYWORDS EST. SOURCE tomato. ORGANISM Lycopersicon esculentum	bukaryota virianplancae; Streptophyta; Emryophyta; Encheophyta; Spermatophyta; Magnollophyta; Encheophyta; Magnollophyta; Encheons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.  REFERENCE I (bases 1 to 593) AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., S. D. S. D. S.	TITLE Generation of ESTs from germinating tomato seed JOURNAL Unpublished (2000) COMMENT CONTECT: CUGI Clemson University Genomics Institute Clemson University
	199 pGluAlaLeuMetAsnGluLeuLySGluValLySGluIleAlaLySProAsnGlu-IleM 21	VY 219 elleuvalvalaspermethicayolnaspalavalashaalusernesapa 239  Db 479 TITTCGFAGTTGACTCTATGACGAGGAGGATCCTGTGAATCCAGCAAAGCTTTCAACG 538  Qy 239 spGlnLeuAsp-ValThrGlyValThrLeuThrLysleuAspGlyAspThrArg-GlyGl 258	Db 539 ATGTCCTTAATTATAAGGGTGGTGTTCTTACTAAATTAGATGGTGGTGGTGG 598  Qy 258 yalaalaeuserileargser-ValthrGlhuysproileLyspheVal-GlyMetSer 277	Db 599 GGCCGCATAACATCCGTTCCGGTAGTAAAACCAATTAAGTTAATTTTCTACCGGT 658  Qy 278 GlulysLeuaspGlyLeuphe 286  Db 659 GAGAAAACGACCTCTGGGATATTTT 685	RESULT 8 BE432304 LOCUS BE432304 605 bp mRNA linear EST 18-MAY-2001 DEFINITION EST398833 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA		ORGANISM Lycopersion esculentum  Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;	Lycopersicon.  Lycopersicon.  AUTHORS 1 (bases 1 to 605)  AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,J.E.,  Liang,R., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,  Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley	, S.D. TITLE Generation of ESTs from tomato fruit tissue, breaker stage JOURNAL Unpublished (2000) COMMENT Contact: CUGI	Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html	FEATURES Location/Qualifiers  Source //organism="Lycopersicon esculentum" //organism="Lycopersicon esculentum"	/db_xref="taxon:4081" /clone="clbG7M%" /clone=lib="taxon:40 breaker fruit, TIGR" /tissue_type="Pericarp" /dev_stage="Pericarp" //dev_stage="neaker"	/dab_lost="Souk" //dab_lost="Vector: pBluescriptSKmcUadapt; Site_1: EccR1; //note="Vector: pBluescriptSKmcUadapt; Site_1: EccR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."  BASE COUNT 190 a 97 c 159 g 159 t to freezing the pericarp."	Alignment Scores: Pred. No.: 3.86e-52 Length: 605 Score: 562.50 Matches: 105 Percent Similarity: 75.25% Conservative: 47 Best Local Similarity: 51.98% Mismatches: 49

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 581)
Walbot, V.
*γου35Ε06.x1 496 - stressed shoot cDNA library from Wang/Bohnert
lab Zea mays cDNA, mRNA sequence.
A1977909
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                                                                                                                                                                                                                      Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /close_lib="496 - stressed shoot cDNA library from Wang/Bohnert lab"
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Tel: 650 723 22227
Tes: 650 725 8221
Email: walbot@stanford.edu
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/lab_host="B.coli XL Gold"
/note="Organ: shoot; Vector: |
Wang/Rohnert"
93 c 161 g 150 t
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Department of Biological Sciences
Stanford University
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/cultivar="B73"
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                                                                                                                                                              /clone_lib=_tomato germinating seedlings, TAMU"
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/note="Vector: pBlueScript SK(-): Site_1: EcoRI; Site_2:
Xhol; 7 days post imbilition on water-agar. Mixed stage
whole germinating seedlings from seed coat emergence up
for two centimeters in seeds not showing obvious signs of
a 97 c 159 g 146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 GlnLeuGlnThrValGlyLysGlnIleAspIleProValTyrSerGluGlyAspGlnVal 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 LeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAlaLeuSerIleArgSerValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 Jordan Hall, Clemson, SC 29634, USA
Smail: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 SerPheThrLeuAspAspPheLeuGluGlnLeuAspGlnValLysAsnLeu 344
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                                                                                                        esculentum,
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Mismatches:
Indels:
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Matches:
                                                                                                   /organism="Lycopersicon/cultivar="TA496"
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                                                                                                                                   /db_xref="taxon:4081"
/clone="cLE15G22"
                                                                   Location/Qualifiers
1. .593
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558.00
76.148
52.798
24.54%
                                                       prime sequence.
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                                                                                                                                                                                                                                                                                                  191
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                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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Query Match:
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AI977909
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HTC 25-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC; clade; Panicoideae; Andropogoneae; Zea.
I (bases I to 1200)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
                                                                                                           332 GCTTTGGTCACAATTCAATCTCGAAATTGGAATTACTGGTGCCATCTTGACGAAGCTA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                292 AlaSerArgIleLeuGly-MetGlyAspValLeuSerLeuIleGluLysAlaGlnGlnAs 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::: ||||||| ||||:::::|||||||:::
                        172 IleValThrAsnAlaLeuLysHisAlaLysGluGluHisLeuAspPheValIleIleAsp 191
                                                                                                                                                                    192 ThrAlaGlyArgLeuHisIleAspGluAlaLeuMetAsnGluLeuLysGluValLysGlu 211
                                                                                                                                                                                                                                                   212 IleAlaLysProAsnGluIleMetLeuValValAspSerMetThrGlyGlnAspAlaVal 231
                                                                                                                                                                                                                                                                                                                                      232 AsnValAlaGluSerPheAspAspGlnLeuAspValThrGlyValThrLeuThrLysLeu 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 pValAspGlnGluLysAlaLysAspLeuGluLysLysMetArgGluSerSerPheThrLe 331
152 ValGlyLysGlnIleAspIleProValTyrSerGluGlyAspGlnValLysProGlnGln 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA Location/Qualifiers 1.1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="this sequence is part of a project of BST assemblies resulting from the application of public
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="PC0070230"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
                                                                                                                                                                                            252 AspGlyAspThrArgGlyGlyAlaAlaLeuSerIleArgSerValThrGlnLysProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysPheValGlyMetSerGluLysLeuAspGlyLeuGluLeuPheHisProGluArgMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512 GCTGGACGTATTTTAGGAAATGGGAGATGTTCTATCGTTTGTTGAGAAAGCCCCAAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      632 CAATGACTTCCTGAAGCAAACTCCGGCAGTTGCTAGGATGGGT 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
/db_xref="MaizeDB:633818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays PCO070230 mRNA sequence. AY109321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY109321.1 GI:21212876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Overgo Probes
Unpublished (2002)
2 (bases 1 to 1200)
Coe,E.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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VERSION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fruit
                                                                                                                                                                                                                                                                                                                                                        BM413418 677 bp mRNA linear EST 22-JAN-2002 EST587745 tomato breaker fruit Lycopersicon esculentum cDNA clone cLEG63C14 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 677)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning, C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescriptSKmcUadapt; Site_1: EcoR1; Site_2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum Bukaryota, Embryophyta, Tracheophyta; Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae, euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                    361 GTACCAGTTTACTCAGAAGGAACTGAAGCAAAACCTTCACAAATAGCCAAAAAGGGTTG 420
                                                                                     LysHisAlaLysGluGluHisLeuAspPheValIleIleAspThrAlaGlyArgLeuHis 197
                                                                                                                                            198 IleAspGluAlaLeuMetAsnGluLeuLysGluValLysGluIleAlaLysProAsnGlu 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677
101
46
47
1
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voiltivaz="TA466"

/db_xref="taxon:4081"

/clone="cLBG632C14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tomato breaker fruit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                       541 GTTCTTCTTGNGGTTGATGCCATGACTGGCCAAGAAGCT 579
                                                                                                                                                                                                                                 218 IleMetLeuValValAspSerMetThrGlyGlnAspAla 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1-677)
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                                                                                                                                                                                                                                                                                                                                                                                                                        BM413418
BM413418.1 GI:18265048
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534.00
75.38%
51.79%
23.48%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tomato.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
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                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                RESULT 11
BM413418
                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
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1 (bases 1 to 533)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Opton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
Unpublished (1999)
                     Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Wector: pBlueScript SK(-); Site_1: BcoR1; Site_2: Xho1; CLEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyLeuGlnGlyalaGlyLysThrThrThrAlaGlyLysLeuAlaLeuLeuMetArgLys 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysTyrAsnLysLysProMetLeuValAlaAlaAspIleTyrArgProAlaAlaIleAsn 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 AAGCAGGGTAAGAGTTGCATGCTGAAGAGGGGGTACAGACCTGCTGCTATTGAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysProGlnGlnIleValThrAsnAlaLeuLysHisAlaLysGluGluHisLeuAspPhe 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GICATAAIGGATACAGCTGGAAGACTICAGATAGATAAAACTATGATGGATGAATTAAAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 GluValLysGluIleAlaLysProAsnGluIleMetLeuValValAspSerMetThrGly 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 GlnAspAlaValAsnValAlaGluSerPheAspAspGlnLeuAspValThrGlyValThr 247
                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="fruit perioarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                              100 Jordan Hall, Člemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                /clone="clbF40N15" /clone_lib="tomato fruit mature green, TAMU"
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AW930742.
contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

1 216 c 317 g 279 t 1 others
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71 CAAGAAGCAGCAGCAATAGTCAACATATTGAGATTGGTATAACTGGTGCAATA 130
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SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

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Sorghum.
Sorghum bicolor
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (Dases 1 to 514)
Sudman, M. and Pratt, M.-M., Gingle, A., Fang, G.C., Dean, R., Wing, R.,
Sudman, M. and Pratt, L.H.
An EST database from Sorghum: plants infected with a compatible pathogen.
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Pel: 706 542 180
                                              3 PheGluGlyLeuSerGluArgLeuGlnAlaThrMetGlnLysMetArgGlyLysGlyLys 22
                                                                                                                                       23 LeuThrGluAlaAspIleLysIleMetArgGluValArgLeuAlaLeuPheGluAla 42
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192 GAIGTTAGCCTTCCTGTTGTAAGAAGATTCGTTCAAACTGTAAGTGAACAAGCTGTGTGT
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US-09-943-108A-2 (1-455) x BQ996389 (1-677)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
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TAG_IBSOF_flowers pre-fertilized
TAG_IBSOF_flowers pre-fertilized
TAG_IBSOF_cCTGGGGGGG"
                                                                                                                                                                                                                                                       рдуурану 677 bp mRNA linear EST 22-AUG-2002 0GG1ZL07. yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone QGG1ZL07, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,T., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig5305, see http://cgpdb.ucdavis.edu/
                                      248 LeuThrLysLeuAspGlyAspThrArgGlyGlyAlaAlaLeuSerIleArgSerValThr 267
                                                                   GlnLysProlleLysPheValGlyMetSerGluLysLeuAspGlyLeuGlu 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Contact: Alexander Kozik [R.W.Michelmore Lab
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Fax: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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/clone_lib="QG_EFGHJ lettuce serriola"
/lab_host="E.coli"
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Mismatches:
Indels:
Gaps:
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Matches:
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/cultivar="L.serriola"
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Plate: QG612 row: L column: 07.
Location/Qualifiers
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source

FEATURES

BASE COUNT

ORIGIN

Pred. No.:

Score:

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Colletotrichum graminicola"

Colletotrichum graminicola"

Note="Vector: pBuescript II SK(-) from Lambda Zap II;
Site_1: XhOi; Site_2: BcoRI; Four-week-old sorghum
seedilings were sprayed with spore suspension prepared from
3-week-old FRW42I, a sorghum isolate of the anthracnose
pathogen Colletotrichum graminicola. Incoulated plants
were kept in a 25 c dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/12 hr of light/dark
cycle at 25 c with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTs are expected to derive
from the host plant, no effort was made to eliminate ESTs
deriving from the pathogen."
below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement. Seq primer: JEN REV High quality sequence stop: 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 PheLeuGluGlnLeuAspGlnValLysAsnLeuGlyProLeuAspAspIleMetLysMet 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspThrArgGlyGlyAlaAlaLeuSerIleArgSerValThrGlnLysProIleLysPhe 273
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                                                                                                                                                                                                                                         /clone_lib="Pathogen-infected compatible 1 (PIC1)"
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                                                                                                                                                                                                                                                             /tissue_type="Leaves"
/dev_stage="4-week-old seedlings infected with
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                       /organism="Sorghum bicolor"/cultivar="BTx623"
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                                                                                                                                                                                                                    /db_xref="taxon:4558"
                                                                                                                              Location/Qualifiers
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485.00
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Tue Feb 25 08:37:14 2003

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February 21, 2003, 15:13:23 ; Search time 40 Seconds (without alignments) 1515.726 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		S. aureus ffh prot	Staphylococcus aur	Staphylococcus aur	Staphylococcus anr	Listeria monocytog	Staphylococcus epi	Enterococcus faeca	Enterococcus faeca	Lactococcus lactis	Streptococcus pneu
		TD CI		AAY00910	AAU37473	AAU33924	AAU36535	ABB49131	ABP39950	AAU33449	AAU35268	ABB54962	AAU37661
				20	22	22	22	23	23	22	22	23	22
		Match Length DB		455	455	455	455	450	338	472	477	518	523
ф	Query	Match	1111111	99.7	99.4	98.3	98.3	75.5	67.5	62.4	62.4	57.8	57.5
		Score		2267	2261	2235	2235	1717.5	1534	1418.5	1418.5	1315	1307
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Streptococcus pneu (DES 28 protein seq CFE 28 protein seq CFE 28 protein seq S. aureus ffh prot Streptococcus pneu Streptococcus poly Streptococcus publication of Streptococcus poly Streptococcus poly Streptococcus poly Strephyloric otopias poly Streptococcus poly Strephyloric cytopias poly Strephyloric cytopias poly Strephylococcus poly Strephyloco	ALIGNMENTS  455 AA.  ce.  tparticle, SRP; antimicrobial agent, vaccine; therapy; infection; otitis media; syndrome; septic arthritis.  syndrome; septic arthritis.  gnal Recognition Particle (SRP) with components - the SRP gene and protein
AAU37932 AAM01025 AAY09165 AAV79165 AAC79165 AAC79167 AAC79167 AAC791817 AAC791817 AAC791817 AAC791817 AAC791819 AAC791819 AAC791819 AAC740110	ALIGNMI 455 AA. 455 AA. 10ce. 1 particle; 2 therapy; syndrome; cynal Recoc
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	RESULT 1 AAYO0910 ID AAYO XX AC AAYO XX DT 28-N XX DE S. a XX XX XX XX XX XX XX Pfh PN EP90 XX XX PN PD 17-N XX XX PN PN PN PN PN PN PN PN PN PN XX XX PN PN PN PN XX XX PN PN PN PN PN PN PN XX XX PN PN PN PN PN PN PN PN PN PN PN PN PN

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                                                                      This sequence is the Staphylococcus aureus signal recognition particle (SRP) fih component. Fih polynucleotides are useful for diagnosing a disease related to expression of fih polypeptides by analysing for the presence/amount of fih protein in a sample due to infection of a micro-organism with the gene, or determining the nucleic acid sequence encoding fih. Fih polypeptides and antagonists are useful for treatment of an individual in need (polypeptides are useful for inhibit (antagonist) fih polypeptide levels. Fih polypeptides and antagonists by binding and observing the affect of fifth polypeptide activity, which are potential anti-microbial agents. Fih polypeptides and antigenic fragments are also useful for inducing an immunological response (T cell/antibody) to protect against disease, by direct administration (vaccine), or via a vector (gene therapy). Anti-fih antibodies are useful as antagonists, and for protecting against disease. Diseases diagnosed, prevented and treated include those caused by infection, especially bacterial infection, include those caused by infection, especially bacterial infection, and including outlis media, conjunctivitis, toxic shock syndrome, wound are useful for bathing wounds and implants prior to surgical
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  ynostic reagents and for prevention and treatment of infections which cause otitis media, septic arthritis
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Pred. No. 2.5e-174;
0; Mismatches 1;
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 and for
                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU37473 standard; Protein; 455 AA
useful as diagnostic reagents
                                                                                                                                                                                                                                                                                                                                                                   99.7%;
                                                  Claim 11; Page 29-30; 35pp;
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                           and toxic shock syndrome
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les 454; Conserv
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               Staphylococci
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Matches
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AAU37473
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are preunohase, Pseudomonas acrupinosa and Enterococcus facalls. The preunohase, Pseudomonas acrupinosa and Enterococcus facalls. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WiPo at.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr GJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
Staphylococcus aureus cellular proliferation protein #1643.
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                                                              Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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Pred. No. 7.5e-174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Seq ID No 13066; 511pp; English.
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2000US-253625P.
2000US-257931P.
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99.3%;
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2000US-207727P.
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                                                                                                                                                                    Staphylococcus aureus
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22-DEC-2000;
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26-MAY-2000;
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Antisense, prokaryotic cellular antibiotic; antibacterial; drug
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2000US-207727P.
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26-MAY-2000;
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Matches 447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aurens, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
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                     181 KEEHLDFVIIDTAGRLHIDEALMNELKEVKDIAKPNEIMLVVDSMTGQDAVNVAESFDDQ 240
                                                                   LDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD
KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ
                                              LDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERNASRILGMGD
                                                                                           VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM
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2000US-206848P.
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2000US-242578P.
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2000US-257931P.
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Xu HH;
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Yamamoto RT,
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23-MAY-2000;
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The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                            98.3%; Score 2235; DB 22;
ilarity 98.2%; Pred. No. 9.5e-172;
Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 NDMKKMMKQFTGGGKGKKGKRNQMQNMLKGMNLPF 455
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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and blodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene, expression and cell replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and modulate L. monocytogenes related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Cherouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Cominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                                                               Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.5%; Score 1717.5; DB 23; Length 450; 72.7%; Pred. No. 4.8e-130; ive 64; Mismatches 55; Indels 5;
          Claim 6; SEQ ID No 1836; 192pp; French.
                                                                                                                                                                                                                                                                                                                Listeria monocytogenes protein #1835
                                                                                                                                                          ABB49131 standard; Protein; 450 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2000; 2000FR-0004629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dominguez-Bernal G, Garridd
Chakraborty T, Domann E, F
Perez-Diez J, Baquero F, G
Maduenio E, De Pablos B, M
Rose M, Voss H;
                                                                                                                                                                                                                                                              (first entry)
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Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes.
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                                                                                                                                                                                                                                                              05-FEB-2002
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                                                                                                                                                                                                               ABB49131;
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                               421
                                                                                                           RESULT 5
                                                                                                                                   ABB49131
                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen a wide variety of organisms. The present sequence is also useful to screen essential prokaryotic cellular proliferation protein.

So wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Wote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from MIPPO at the contract of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENISINMSNKPPTVVMMVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAFEGLSERLQATMQKWRGKGKLTEADIKIMMREVRLALLEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAPEGLSERLQAIMQKMRGKGKLIEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
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                                                                                                                                                                                                                                                                                                                                  New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.3%; Score 2235; DB 22; Length 455; 98.2%; Pred. No. 9.5e-172; ive 3; Mismatches 5; Indels 0
                                                                                                                                                                                  Trawick JD,
                                                                                                                                                                               Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDMKKMMKQFTGGGKGKKGKRNQMQNMLKGMNLPF 455
                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Seq ID No 12128; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                    2000US-253625P.
2000US-257931P.
2000US-242578P
                                                                            2001US-269308P
                                                                                                                                                                               Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 447; Conservative
                                                                                                                             (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                         Xu HH;
                                                                                                                                                                                                                                                         2001-611495/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455 AA;
                                                                                                                                                                                                                                                                                   N-PSDB; AAS54394.
                       27-NOV-2000;
22-DEC-2000;
                                                                            16-FEB-2001;
                                                                                                                                                                             Haselbeck R,
Yamamoto RT,
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPPTO web site.
                                                                                                                                                                                                                                                                          66 LGSDVMQSLTPGQQVIKIVQEELTSLMGGENTSIKWANKPPTVVMMVGLQGAGKTTTAGK 125
                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LGSDYMQSLTPGQQVIKIYQDELTKLMGGENTSINMSNKPPTVVMMYGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                      121 LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                             LDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300
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                                                                                                                                                             Gaps
                                                                                                                                                                                                                         6 MAFEGLSDRLQATMQKMRGKGKVTEADIKTMMREVRLALLEADVNFKVVKEFVKNVSERA 65
                                                                                                                                                                                                                                                                                                                                                                                 KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ
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                                                                                                                                                               ;
0
                                                                                                                                 Length 338;
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                                                                                                                                                               Indels
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                                                                                                                                23;
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                                                                                                                                Query Match 67.5%; Score 1534; DB 22
Best Local Similarity 92.5%; Pred. No. 2e-115;
Matches 307; Conservative 16; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU33449 standard; Protein; 472
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-253625P.
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Xu HH;
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N-PSDB; AAS51308.
                                                                                                  338 AA;
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
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16-FEB-2001;
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                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                 181
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ID AAU3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to
                                                                                                                                                                                             240
                                                                     120
                                                                                                    180
                                                                                                                   240
                                                                                                                                                                                                                          LDVTGVTLITKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300
                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                       VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM 360
                                                                                                                                                                                                                                                                                                       420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
        09
                                                                                                                                                                                                                                           LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA
                                                                                                                                                                                 MAFEGLAGRLQETMNKIRGKGKVNEADVKEMMREVRLALLEADVNFKVVKQFIKTVSERA
                                       LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK
                                                           KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ
                                                                                                                                                                                                                                                                                                                                                  KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4795
                                                                                                                                                                                                                                                                                                                                                                                                                                 NDMKKMMKQFTGGGKGKKKKRNQMQNMLKGMNLFF 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID 4795; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP39950 standard; Protein; 338 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis; antibacterial; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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N-PSDB; ABN92495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUL-2002
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scenariolia coli, staphylococcus aureus, Salmonella typhi, Ribabiella premoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets or antibiotic development. The antissense nucleic acids can also be used to infentify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins, the programmes. The antissense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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Enterococcus faecalis cellular proliferation protein #555
                                            Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Seq ID No 10861; 511pp; English.
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2000US-207727P.
2000US-242578P.
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20000S-257931P.
20010S-269308P.
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                                                                                                                    Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                                                 23-MAY-2000;
26-MAY-2000;
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22-DEC-2000;
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                                                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotse used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, pseudomonas aeruginosa and Enterococcus facealis. The promarion is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention is also useful for the identification, to express these proteins. Community proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Cof the printed specification, but was obtained in electronic form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.4%; Score 1418.5; DB 22; Length 472; 59.0%; Pred. No. 6.5e-106;
ive 86; Mismatches 89; Indels 15;
                        for the identification and development of
                        New polynucleotides for the identification and development
antibiotics, comprise sequences of antisense nucleic acids
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                                                                                        Example 3; Seq ID No 4945; 511pp; English.
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Matches 273; Conservative
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                                                                                                                            1 MAFENLTERLQNVFKNLRGKKKITETDVTEITKEIRVALLBADVALPVVKKFIKAIRERA
                                                          KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae cellular proliferation protein #90.
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2000US-253625P.
2000US-257931P.
2001US-269308P.
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27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                 241 LGITGVVITKMDGDTRGGAALSIRAVTGAPIKFVGSGEKLTDLEIFHPDRMSSRILGMGD 300
                                                                                                                            301 VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM 360
                                                                                                                                                                                                  361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                                                                                                     361 PGIENVKVDPKDVARKRAMVLSMTPAERENPDLINPSRRRIAAGSGNSVVEVNRMIKQF 420
                                                      LDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleotide sequence useful in the identification or Lactococcus lactis and related species \mbox{\, \cdot \,}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.8%; Score 1315; DB 23; Length 518; 55.4%; Pred. No. 1.6e-97; ive 88; Mismatches 102; Indels 18.
                                                                                                                                                                                                                                                                                             : ||||:| : | || |:| 421 KESKKMMQQMSKGDMNIPGMDQMLGGGVKGKLGKM-AMNRMMK 462
                                                                                                                                                                                                                                                                         NDMKKMMKQFT------GGGKGKKCKRNQMQNMLK 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlich SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; SEQ ID No 1664; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorokine A, Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                ABB54962 standard; Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis protein ffh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000FR-0004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2000; 2000FR-0004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis IL1403.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-043418/06.
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les 258; Conserv
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11-APR-2000;

Bolotine A,

Query Match Best Local S Matches 258

δy

Sequence

FR2807446-A1.

ABB54962;

12-OCT-2001

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                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                        programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO.
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PALQNMKVDERQIARKRAIVSSWIPPERENPDLLNPSRRRRIAAGSGNTFVEVNKFIKDF 420
                                                                                                                                                                                                                                                                                                                                                                                                                          LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDVIGVILIKLDGDIRGGAALSIRSVIQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEVIGVILIKIDGDIRGGAALSVRHIIGKPIKFIGIGEKIIDLETFHPDRMSSRILGMGD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLTLIEKASQEYDEQKALEMAEKMRENTFDFNDFIDQLDQVQNMGPMEDLLKMIPGMANN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                               1 MAFESLIERLONVFKNLRKKGKISESDVQEATKEIRLALLEADVALPVVKDFIKKVRERA 60
                                                                                                                                                                                                                                                                                                                                                                   1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ
                                                                                                                                                                                                                                                                                                                Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae cellular proliferation protein #361.
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic cellular proliferation protein;
antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                         90; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NQAKQLMQGVMSG-----DMNKMMKQMGINPNNLP 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDMKKMMKQFTGGGKGKKKKRNQMQNMLKGM-----NLP 454
                                                                                                                                                                                                                                                                                                   57.5%; Score 1307; DB 2:
                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU37932 standard; Protein; 466 AA.
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                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                   523 AA;
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                                                                                                                                                                                                                                                                                                                            Sest Local Simi
Matches 253;
                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are schemically staphylococcus aureus, Salmonella typhi, Klebsiella promuoniae, Pseudomonas aeruginosa and Enterococus faccalis. The prokaryotic development. The antisense nucleic acids can also be used to antibiotic development. The antisense nucleic acids can also be used to chemity proteins used in proliferation, to express these proteins.

The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen to homelogous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

The printed specification, the present sequence represents an essential prokaryotic cellular proliferation protein.

Wote: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                      Carr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAFESLTERLONVFKNLRKKGKISESDVQEATKEIRLALLEADVALPVVKDFIKKVRERA
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                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 7.5e-97
1; Mismatches 10:
                                                                                                                                                                                                                                                                                                                                                                                                                      Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind
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54.9%; Pre
tive 91;
                                                                                                                                                                          2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                     21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                .6-FEB-2001; 2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen KL,
Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-611495/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS55791
WO200170955-A2.
                                                                                                                                                                             23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                      Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto RT,
                                                    27-SEP-2001
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Matches 252;
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523 AA;

Sequence

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ris pressor, invention teaches to include a data (which are essential for the viability of a bacterial cell wall. The acronym CFE stands for "CEG For Expression", where CEG stands for "Conserved Essential Gene". The nucleic acids are useful for detecting the presence of proteins essential for the viability of a bacterial cell wall in samples such as cells, tissues, blotogical fluids, blood, serum, nose, ear or throat swabs with ligands, and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nucleic acids are also useful for determining whether a genomic nucleic acids are also useful for determining whether a genomic nucleic desequence of interest is essential for viability of a bacterial cell or whether it resides within an operon, by integrating an exogeneous nucleotide sequence of interest comprising 20°-500 base pairs) into the genomic sequence of interest which confers a selection agent such as chloramhenicol. The nucleic cell cidentification of showers and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids antibiotic resistant bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding conserved essential genes involved in bacterial replication which are potential targets for the treatment of antibiotic
301 VLSLIEKAQQDVDQEKAKDLEKKARRSSFILDDFLEQLDQVKNLGPLDDIMKAIPGNNKM 360 :|:|||||| |: |::||| :: :|||||||
                       420
                                                                                                     Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE; CEG; Conserved Essential Gene; bacterial infection; antisense therapy; antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davison DB, Bruccoleri RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to nucleic acids (AAH90701-AAH90918)
                                                                                361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF
                                                                                                                                                                                                  421 NOAKQLMQGVMSG-----DMNKMMKQMGINPNNLP 450
                                                                                                                                                            421 NDMKKMMKQFTGGGKGKKGKRNQMQNMLKGM-----NLP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dougherty TJ, Pucci MJ, Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Pages 265-267; 380pp; English.
                                                                                                                                                                                                                                                                                                   AAM01025 standard; Protein; 523 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resistant bacterial infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-2000; 2000WO-US35604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0174089
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                       CFE 28 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-496721/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAH90724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200149721-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thanassi JA;
                                                                                                                                                                                                                                                                                                                                                                               02-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-2001
                                                                                                                                                                                                                                                                                                                                           AAM01025;
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Ffh gene; signal recognition particle; SRP; antimicrobial agent; vaccine; immunological response; gene therapy; infection; otitis media; conjunctivitis; toxic shock syndrome; septic arthritis.
                                                                                                                                                                                                                                                                                                                                                                       180
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                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                     241 LDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300
                                                                                                                                                                                                                                                                                                      VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKW 360
                                                                                                                                                                                                                                                                                                                      420
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                                                                                                                 Gaps
                                                                 1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA
                                                                                                   LGSDVMQSLTPGQQVIKIVQDELTKIMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK
                                                                                                                                                   LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA
                                                                                                                                                                                                   181 KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ
                                                                                                                                                                                                                  361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Staphylococcus aureus Signal Recognition Particle (SRP) with protein (ffh) and RNA (ffs) components - the SRP gene and protein useful as diagnostic reagents and for prevention and treatment of
                          14;
Length 523;
                         Indels
57.4%; Score 1306; DB 22;
54.9%; Pred. No. 8.8e-97;
ive 91; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                         421 NQAKQLMQGVMSG------DMNKMMKQMGINPNNLP 450
                                                                                                                                                                                                                                                                                                                                                                                                         421 NDMKKMMKQFTGGGKGKKGKRNQMQNMLKGM-----NLP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY00911 standard; Protein; 264 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. aureus ffh protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98EP-0306741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-169238/15.
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX27222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1998;
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                         Matches 252;
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  Query Match
               Local
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98EP-0306685.

20-AUG-1998;

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This sequence is the Staphylococcus aureus signal recognition particle (SRP) fife Component. Fife polynucleotides are useful for diagnosing a disease related to expression of fife polypeptides by analysing for the presence/amount of fife protein in a sample due to infection of a micro-organism with the gene, or determining the nucleic acid sequence encoding ffh. Fife polypeptides and antagonists are useful for treatment of an individual in need (polypeptide) of, or needing to inhibit (antagonist) fife polypeptides and antagonists are useful for identifying agonists and antagonists by binding and observing the affect of fife polypeptide activity, which are polypucleotides are useful for identifying agonists and antagonists by binding and observing the affect of fife polypeptide activity, which are constituted anti-incrobial agents. Frh polypeptides and antigonists by binding and observing the affect of fife polypeptides and antigonists, are also useful for inducing an immunological response (T cell/antibody) to protect against disease, by direct administration (vaccine), or via a correct against disease. Diseases diagnosed, prevented and treated include those caused by infection, especially bacterial infection, include those caused by infection, especially bacterial infection, and infection and septic arthritis. Futh polypeptides are antimicrobial, and are useful for bathing wounds and implants prior to surgical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMNVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAFEGLSERLQATMOKNRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAFEGLSERLQATMOKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae; ffh; fifty-four homologue; antibacterial; infection; otitis media; conjunctivitis; bacteraemia; sinusitis; pleural empyema; endocarditis; meningitis.
Staphylococci infections which cause otitis media, septic arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVINALKFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.4%; Score 1305; DB 20;
llarity 100.0%; Pred. No. 4.1e-97;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae ffh protein.
                                                                   Claim 11; Page 31-32; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW99658 standard; Protein; 523 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDVTGVTLTKLDGDTRGGAALSIR 264
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                      and toxic shock syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 264; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW99658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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The present sequence represents the Streptococcus pneumoniae fifty-four homologue (ffh) protein, which is a component of the protein secretory apparatus in Bacteria, and the bacterial homologue of the eukaryotto Signal Recognition Particle. Fifth proteins and polynucleotides are useful of diagnosing diseases related to over or underexpression of Ffh protein or instances of the eukaryotta of the Fff gene, or determining Ffh protein or mRNA expression levels due to an infection of an organism with the Ffh gene. They can diagnose the stage and type of infection. Ffh proteins are also useful for screening for compounds which affect activity of the protein by measuring the binding to fifth protein and observing the stimulation or inhibition of the protein function. These can be used in treatment to inhibit (antagonist i.e. antibacterial drugs) or enhance cannotist. Ffh activity, in addition to direct administration of Ffh proteins (administration of antisense sequences to prevent expression. Ffh proteins (administration of antisense sequences to prevent expression. Ffh proteins (administration of antisense sequences to prevent disease. Content and as a vaccine) and antibodies induce an immune response to immunise and prevent disease. Conjunctivitis, bacteraemia, sinusitis, pleural empyema, endocarditis and especially meningitis. Ffh proteins, polynucleotides and their conjunctivitis, bacteraemia, sinusitis, pleural empyema, endocarditis and especially meningitis. Ffh proteins, polynucleotides and their can prevent adhesion of bacterial to prevent bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVABSFDDQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 IDVTGVTLTKIDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAFESLTERLONVFKNLRKKGKISESDVQEATKEIRLALLEADVALPVVKDFIKKVRERA 60
                                                                                                                                                                                                                                          New Streptococcus pneumoniae Fifty-Four Homologue (Ffh) polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of Streptococci infections, which cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAPEGLSERIQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.0%; Score 1297; DB 20;
54.7%; Pred. No. 4.7e-96;
live 91; Mismatches 103;
                                                                                                                                                                                                                                                                                                            otitis media, sinusitis and conjunctivitis
                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 6; 21pp; English.
                                            97US-0923772
                                                                                        (SMIK ) SMITHKLINE BEECHAM.
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Matches 251; Conservative
                                                                                                                                                                         WPI; 1999-155936/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           523 AA;
                                                                                                                                                                                                 N-PSDB; AAX19484
                                            02-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection
                                                                                                                                    Black MT;
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                                                                                                                                                                                                                                                                                                                                                                                                                 "Optionally (R2)n-Y, where R2 is any amino acid residue, n is an integer between 1 and 1000 and Y is a hydrogen or a metal"
                 361 KGLDKINMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAFEGLSERLQATMQKMRGKGKLfEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Gaps
                                                                                                                                                                                                                                                              Fifty-four homologue; ffh; bacterial infection; Staphylococcus aureu
Streptococcus pneumoniae; wound treatment; antibacterial; vulnerary
                                                                                                                                                                                                                                                                                                                                                               R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treatment of bacterial infection using modulators of the fifty-four
                                                                                                                                                                                                                                                                                                                                                            /note= "Optionally X-(Rl)n, where X is hydrogen, is any amino acid residue and n is an integer between 1 and 1000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.0%; Score 1297; DB 23; Length 523; 54.7%; Pred. No. 4.7e-96;
                                                                                                                                                                                                                                     Streptococcus pneumoniae fifty-four homologue (ffh) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ľ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 251; Conservative 91; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
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                                                                      NDMKKMMKQFTGGGKGKKGKRNQMQNMLKGM----NLP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologue protein of Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Payne
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                    AAU79163 standard; Protein; 523 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BEECHAM CORP. BEECHAM PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001GB-0007127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2000; 2000US-191008P.
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cheever C, Fecteau D,
                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 523
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Job time : 44 secs
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3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/FG_COMB.pep:*

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US-08-317-401E-4

US-08-317-401E-4

US-08-317-401E-4

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US-08-131-0010-4817

US-09-134-001-481-2

US-09-107-478-1

US-09-107-484-4

US-09-107-484-4

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US-09-107-484-4

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Copyright (c) 1993 - 2003
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Listing first 45 summaries

    protein search, using sw model

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Sequence 112, Appli
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Sequence 5218, Ap
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   Sequence
              Seguence
                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09035382

Patent No. 6284515
GENERAL INFORMATION:
APPLICANT: Black, Michael T.
TITLE OF INVENTION: SIGNAL RECOGNITION PARTICLE POLYPEPTIDES
TITLE OF INVENTION: AND POLYNUCLEOTIDES
TITLE OF INVENTION: AND POLYNUCLEOTIDES
CURRENT FILIAME DATE: 1998-03-05
GURRENT FILIAME DATE: 1997-09-03
MUMBER: OF SEQ ID NOS: 8
SOLTWARE: FASTERE OF Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2274; DB 4; Length 455; llarity 100.0%; Pred. No. 1.2e-190; Conservative 0; Mismatches 0; Indels 0
US-08-981-527A-10
US-08-76-265-3
US-08-290-731C-10
US-08-290-731C-6
US-08-291-079-8
US-09-134-001C-4349
US-09-134-001C-4968
US-08-353-700-1
PCT-US95-1621-1
US-08-353-700-1
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US-08-313-856-112
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US-08-313-836-112
US-09-313-001C-3547
US-09-134-001C-3547
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  Best_Local Similarity
Matches 455; Conserv
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52, Appl 4378, Ap

Sequence Sequence Sequence

US-09-134-001C-5080 US-09-315-793-52 US-09-134-001C-4378

5178, Ap 3159, Ap 8, Appli 5080, Ap 52, Appl

, Appli 1, Appl

Sequence Sequence Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGSDYMQSLTPGQQVIXIVQDELTKLMGGENTSINMSNKPPTVVMVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LALLEMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                             1 MAPEGLSERLQATMOKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
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                                                                                                                                                                                                                                   DB 4; Length 264;
                                                                                                                                                                                                                                                                                                Indels
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                               57.4%; Score 1305; DB 4; I
100.0%; Pred. No. 2.5e-106;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GM10080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 LDVIGVILIKLDGDIRGGAALSIR 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-923-772-2
; Sequence 2. Application US/08923772
; Patent No. 5972651
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Black, Michael T. TITLE OF INVENTION: NOVEL ffh NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28,354
                                                                                                                                ORGANISM: Staphylococcus aureus US-09-035-382-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 523 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOS
                                                                                                                                                                                                                                                                                                   Matches 264; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: F
STATE:
                                                                                                                                                                                                                                      Query Match
Best Local &
                                                                                                     TYPE: PRT
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(9-09-134-001C-4795

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(9-09-134-001C-4795)

(9-09-134-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-001C-67-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 LDVSGVTLFKLDGDFRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LGSDVMQSLIPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
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                                     361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 MAFEGLSDRLQATMQKMRGKGKVTEADIKTMMREVRLALLEADVNFKVVKEFVKNVSERA 65
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Patent No. 6264515;
GENERAL INFORMATION:
APPLICANT: Black, Michael T.
TITLE OF INVENTION: SIGNAL RECOGNITION PARTICLE POLYPEPTIDES;
TITLE OF INVENTION: AND POLYNUCLEOTIDES
TILE REFERENCE: GAS0335;
CURRENT FILING DATE: 1998-03-05;
EARLIER APPLICATION NUMBER: 60/057,890;
BARLIER FILING DATE: 1997-09-03;
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.5%; Score 1534; DB 4; Length 338; 92.5%; Pred. No. 3.5e-126;
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                                                                                                     421 NDMKKMMKQFTGGGKGKKGKRNQMQNMLKGMNLPF 455
                                                                                                                                                                      421 NDMKKNMKQFTGGGKGKKGKRNQMQNMLKGMNLPF 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 VLSLIEKAQQDVDQBKAKDLEKKMRESSFTLD 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 307; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-134-001C-4795
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US-09-035-382-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 KGLDKINMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                        1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                                                                                                                                                                                181 KEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQ
                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BELTZ, Gerald A.
COUGHLIN, Richard T.
TITLE OF INVENTION: UNCLEIC ACIDS, PROTEINS, AND METHODS OF USE OF GRANULOCYTIC ERHLICHIA
                                                                                                                                                                                                           Length 523;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/ANS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                         57.0%; Score 1297; DB 4;
54.7%; Pred. No. 3.4e-105;
tive 91; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDMKKMMKQFTGGGKGKKKKRNQMQNMLKGM----NLP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQAKQLMQGVMSG------DMNKMMKQMGINPNNLP 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,047A
                                                                                                                              TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-066-047-8; Sequence 8, Application US/09066047A; Patent No. 6306394; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER/SICS:
LENGTH: 523 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MURPHY, Cheryl STOREY, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                          Best Local Similarity 54.79
Matches 251; Conservative
                                                                                                                                                                     US-09-385-287-2
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                              241 LDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRILGMGD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINNSNKPPTVVMMVGLQGAGKTTTAGK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 KGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF 420
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                                                                                     Gaps
                                                                                                                        1 MAFEGLSERLQATWQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA 60
                                                                                                                                                            1 MAFESLTERLONVEXNLRKKGKISESDVQEATKEIRLALLEADVALPVVKDFIKKVRERA 60
                                                                                   14;
                                          Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                        57.0%; Score 1297; DB 2;
54.7%; Pred. No. 3.4e-105;
iive 91; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQAKQIMQGVMSG------DMNKMMKQMGINPNNLP 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDMKKNMKQFTGGGKGKKKKRNQMQNMLKGM----NLP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/385,287
FILING DATE: 30-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GM10080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEBRAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/923,772
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Black, Michael T. TITLE OF INVENTION: NOVEL ffh NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09385287 Patent No. 6350857 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION
                                    Query Match
Best Local Similarity 54.74
Matches 251; Conservative
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US-08-923-772-2
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US-08-317-401E-2
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US-08-317-401E-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242
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APPLICANT: Thompson, Sheryl Ann
APPLICANT: Twoer, Debbie Sue
TTTLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE OF
TITLE OF INVENTION: ASPERGILLUS NIGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FNSLIKGFSSALQRLSGKREISSKDFDLVIEDITQALLDADVNLGVVDEFIENVKSKIVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKMKGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLM
                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                   37.2%; Score 846; DB 4; Length 420; 40.8%; Pred. No. 6.3e-66; tive 98; Mismatches 143; Indels
                                                                                                                                         REFERENCE/DOCKET NUMBER: 106.941.156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,869
FILING DATE: 25-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Superfo, Colleen
REGISTRATION NUMBER: 39,850
                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
FILING DATE: 24-Apr-1998
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                      LENGTH: 420 amino acids TYPE: amino acid STRANDEDNESS: <Unknown>
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US-08-317-401E-2
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120 KLALLMRKKYNK---KPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 LKHAKEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAES 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDDQLDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRIL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMGDVLSLIEKAQQ-DVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 GLSNLTAGLDDEDGSMK-LRRMIYIFDSMTAAELDGDGKMFVEQPSRMVRIACGSGTTVR 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 ALGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 GM-NKMKGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNV---SRKKRIAKGSGRSLQ 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAFEGLSERLQATMQKMRGKGKLTEAD-IKIMMREVRLALFEADVNFKVVKEFIKTVSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 534;
                                                                                                                                             SOFTWARE: PATENTIN Rolesse #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/317,401E
FILING DATE: 03-October-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 EVNRLMKQFNDMKKMMKQFTGGGKGKKGKRNQMQNMLKGMN 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.8%; Score 586; DB 2; L 33.6%; Pred. No. 4.6e-43; live 75; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 4248.000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEPRA: 212 867 0298
                                                                         S: Floppy disk
IBM PC compatible
NYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08317401E; Patent No. 5922561; GENERAL INPORMATION: APPLICANT: Thompson, Sheryl Ann APPLICANT: Yaver, Debbie Sue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Aspergillus niger
                                                                                                                                                                                                                                                                                NAME: Harrington, James J. REGISTRATION NUMBER: 38,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein ORIGINAL SOURCE:
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Sequence 8, Application US/08981527A

Patent No. 6410262

GENERAL INFORMATION

APPLICANT: Quax, Wilhelmus J.

APPLICANT: Quax, Wilhelmus J.

APPLICANT: Quax, Wilhelmus J.

APPLICANT: Brockhuizen, Cornelis P.

TITLE OF INVENTION: No. 6410262el Secretion Factors for

TITLE OF INVENTION: No. 6410262el Secretion Factors for

TITLE OF INVENTION: G. 6410262el Secretion Factors for

TITLE OF INVENTION: Of Using It

FILE REFERENCE: GCX222-02

CURRENT APPLICATION NUMBER: US/08/981,527A

CURRENT FILING DATE: 1996-07-05

PRIOR FILING DATE: 1996-07-05

NUMBER OF SEQ ID NOS: 20

SECTIONER OF SECTION NOS: 20
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Patent No. 6380370
; GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 LQGAGKTTTAGKLALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQQIVINALKHAKEEHLDFVIIDTAGRLHIDEALMNEIKEVKEIAK-----PNEIMLVV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSWTGQDAVNVAESFDDQLDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 --KIVSERALGSDVMQSLIPGQQVIKIVQDELIKL--MGGENIS-INMSNKPPIVVMMVG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 LKKEVKRR------NIQDPKEVKSVISEKIVEIYNSGDEQISELNIQDGRLAVILLVG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 EGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFE-----ADVNFKVVKEFI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.9%; Score 429.5; DB 4;
34.0%; Pred. No. 1.1e-29;
iive 64; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: GTC-007
CURRENT PLILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FLIXE DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 LELFHPERMASRILGMGDVLSLIEKA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 34.00
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-134-001C-4817
      RESULT 9
JS-08-981-527A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGSDVMQSLTPGQQVIKIVQDELIKLMGGENTSINMSNKPPTVVMMVGLQGAGKITTAGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWIGQDAVNVAESFDDQLDVTGVTLIKLDGDTRGGAALSIRSVTQKFIKFVGMSEKLDGL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 ELPHPERMASRILGMGDVLSLIEKAQQ-DVDQEKAKDLEKKMRESSFTLDDFLEQLDQVK 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;||| : ||||: | ||| : | || 360 KMGPLSKLSGWIPGLSNLTAGLDDEDGSMK-LRRMIYILDSMTAAELDG-DGKNFVEQPS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 GDQVKPQQIVTNALKHAKBEHLDFVIIDTAGRLHIDBALMNELKEVKEIAKPNEIMLVVD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STIGGAAEAQSSAFKATADFGAIIITKTDGHAAGGGAISAVAATHTPIIYLGTGEHLMDL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 NLGPLDDIMKMIPGM-NKMKGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNV----S 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MYLQDLGRRINAAVNDLTRSNNLDEKAFDDMIKEICAALLSADVNVRLVQSLRKSIKSSV 60
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                                                                                      No. 59225610 No. 5922561disk of No. 5922561th America,
    OF.
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    GENES ENCODING SIGNAL RECOGNITION PARTICLE ASPERGILLUS NIGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 552;
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33.5%; Pred. No. 2.4e-42;
Live 75; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) SURENT APPLICATION DAPA:
APPLICATION NUMBER: US/08/317,401E
FILING DAPE: 03-October-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                      STREET: 405 Lexington Avenue, Suite 6400 CITY: New York STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE. DOCKET NUMBER: 4248.000-US
TELECOMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEPAX: 212 867 0298
                                                                                                                                                                     COUNTRY:

2IP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"VOTTER: IBM PC COMPATIBLE

"TOTTER: PC-DOS/MS-DOS
"TOTTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 552 amino acids
amino acid
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                                                                     CORRESPONDENCE ADDRESS
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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LENGTH: 425 amino acids
TYPE: amino acid
                 Query Match
Best Local Similarity 31.48
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 32.55
Matches 105; Conservative
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US-08-986-963-2
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                                                                                                                                                                                    122 ALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAK 181
                                                                                                                                                                                                                                                                                               EEHLDFVIIDTAGRLHIDEALMNELKEVKEIAK-----PNEIMLVVDSMTGQDAVNVAE 235
                                                                                                                                                                                                                                                                                                                                                                 SFDDQLDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPERMASRI 295
                                                                                                                                                               SLTPGQQVI-KIV----QDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGKL 121
                                                                   Gaps
                                                                                                  8 ERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALGSDVMQ 67
                                                                 27;
                             18.8%; Score 426.5; DB 4; Length 415; 31.4%; Pred. No. 2.8e-29; Live 76; Mismatches 122; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
STATE: Philadelphia
STATE: PA
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SOFWARER: FRACEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09007476;
Patent No. 6159949;
GENERAL INFORMATION:
APPLICAT: Black, Michael T.
TITLE OF INVENTION: NO. 6159949el FtsY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 YGLFADMIEQNEDIPEEISRNSSVESEE 413
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TELEPHONE: 215-994-2488
TELEFAX: 215-994-2222
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
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LENGTH: 416 amino acids
TYPE: amino acid
                                              Best Local Similarity 31.4 Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTR: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM IYPE: Diskette
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US-09-134-001C-4817
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                                Query Match
                                                Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDFVIIDTAGRLHIDEALMNELKEVKEIAK-----PNEIMLVVDSMTGQDAVNVAESFD 238
                                                                                                                                                                      97 ONFOEGLNNLIARYRKVDEDFFEALERM---LITADVGFNTV----MTLTEELRMEAQRR 149
                                                                                                                                                                                                                               68 SLTPGQQVIKIVQDELTKLMGGE----NTSINMSNKPPTVVMMVGLQGAGKTTTAGKLALL 124
                                                                                                                                                                                                                                                                                    150 NIQDTEDLREVIVEKIVEIYHQEDDNSEAMNIEDGRLNVILMVGVNGVGKTTTTGKLA-Y 208
                                                                                                                                                                                                                                                                                                                                                                              DQLDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGMSEKLDGLELFHPER----MASR 294
                                                                                                                                                                                                                                                                                                                                             125 MRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKEEH 184
                                                              Gaps
                                                                                                                    ERLOATMOKWRGKGKLITEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERALGSDVMQ
                                                              22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08986963
| Patent No. 5958730
| GENERL INFORMATION:
| APPLICANT: Rosteck Jr., Paul R.
| TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence; NUMBER OF SEQUENCES: 4
| NUMBER OF SEQUENCES: 4
| CORRESPONDENCE ADDRESS:
  Length 416
18.5%; Score 421; DB 4; Length 416
31.4%; Pred. No. 8.4e-29;
ive 78; Mismatches 121; Indels
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MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPUTER: OCCUPACION PC COMPATIBLE
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-11
TELECOMUNICATION INFORMATION:
TELEPHONE: 317/276-3334
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               December 8, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 ILGMGDVLSLIEKAQQDVDQEK 316
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162 SEGDQVKPQQIVTNALKHAKEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAK-----P 215
                                                                                                                                                                                                                                 286 TGPEKADPASVVFDGMERAVARGIDILMIDTAGRLQNKDNLMABLEKIGRIIKRVVPEAP 345
                                                                                                                                                                                                                                                                     216 NEIMLVVDSMTGQDAVNVAESFDDQLDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKFVG 275
                                                                                                                                                                                                                                                                                        227 TVMLFVGVNGVGKTTSIGKLA-HRYKRTGKKVMLVAADTFRAGAVAQLAEWGRRVDVPVV 285
                                                     GSDV------GGENTSINMSNKPP 101
                                                                                                                          102 TVVMMVGLQGAGKTTTAGKLALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09309682 Patent No. 6214348 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          276 MSEKLDGLELFHPERMASRIL 296
                                                                                                                                                                                                                                                                                                                                                                          406 FGEKIDDIGEFNSENFMKGLL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215-994-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4000 L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-09-309-682-2
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ZIP: 19103
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US-09-309-682-2
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                                                                                                                                                                                                                                                                                                           161 LIMSDVGVQVASNLTEELRYEAKLENAKKPDALRRVIIEKLVELYEKDGSYDESIHFQDN 220
                                                                                                                                           100 PPTVVMMVGLQGAGKTTTAGKLALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIP 159
                                                                                                                                                              160 VYSEGDQVKPQQIVTNALKHAKEEHLDFVIIDTAGRLHIDEALMNELKEVKEIAK---- 214
                                                                                                                                                                                                                                      215 -PNEIMLVVDSMTGQDAVNVAESFDDQLDVTGVTLTKLDGDTRGGAALSIRSVTQKPIKF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
2 AFEGLSERLQATMOKMR-GKGKLTEADIKIMMREVRLALFEADVNFKVV-KEFIKTVSER 59
                                                                    60 ALGSDV-----GGENTSINMSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.5%; Score 397.5; DB 3; 32.4%; Pred. No. 9.9e-27; ive 64; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09007484
Patent No. 607203.

GENERAL INFORMATION:
APPLICANT: Black, Michael T.
ATTLE OF INVENTION: No. 6072032el FtsY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GM10081
                                                                                                                                                                                                                                                                                                                                                         274 VGMSEKLDGLELFHPERMASRIL 296
                                                                                                                                                                                                                                                                                                                                                                                  399 IGFGEKIDDIGEFNSENFMKGLL 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Falk. Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10
TELEPHONE: 215-994-2488
TELEPHONE: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
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Best Local Similarity 32.44
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-09-007-484-2
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STATE:
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6 Gaps 4 EGLSERLQATMQKMR-GKGKLTEADIKIMMREVRLALFEADVNFKVV-KEFIKTVSERAL 61 45; Length 430; Indels 3: Dechert Price & Rhoads 4000 Bell Atlantic Tower, 1717 Arch Stre Query Match 17.5%; Score 397.5; DB 4; Best Local Similarity 32.4%; Pred. No. 9.9e-27; Matches 104; Conservative 64; Mismatches 108; COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 APPLICANT: Black, Michael T.
TITLE OF INVENTION: No. 6214348el FLSY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/309,682
FILING DATE:
CLASSIFICATION: GM10081 PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/007,484 NAME: Falk, Stephen T REGISTRATION NUMBER: 36,795 REFERENCE/DOCKET NUMBER: GM] TELECOMMUNICATION INFORMATION: FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Falk, Stephen T LENGTH: 430 amino acids TYPE: amino acid STRANDEDNESS: single 215-994-2488 ã

4 EGLSERLQATMOKMR-GKGKLTEADIKIMMREVRLALFEADVNFKVV-KEFIKTVSERAL 61

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                                                                                                                              :| | :|: |||:|: ||: || :|| 346 HETFLALDASTGQNALVQAKEFSKITPLTGIVLTKIDGTARGGVVLAIREELNIPVKLIG 405
           --ARLNAFFA--NFRSVDEEFFEELEELLI 167
                                                                                  62 GSDV-----GGENTSINMSNKPP 101
                                                                                                                                                                                                                                 TVVMMVGLQGAGKTTTAGKLALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVY 161
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Patent No. 6072032

GENERAL INFORMATION:
APPLICANT: Black, Michael T.
TITLE OF INVENTION: No. 6072032el FtsY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
STATE: PA
COUNTRY: US
COUNTRY: US
COUNTRY: US
COUNTRY: US
COUNTRY: US
COUNTRY: WAS ADDRESSEE FORM:
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33.5%; Pred. No. 2.4e-26;
tive 59; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,484
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 FGEKIDDIGEFNSENFMKGLL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 MSEKLDGLELFHPERMASRIL 296
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 33.55
Matches 92; Conservative
123 ETVQEKYDRSLKKTRTGFG
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linear
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TELEX:
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TOPOLOGY:
US-09-007-484-4
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148 QLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKEEHLDFVIIDTAGRLHIDEALMNELK 207
                                                                      EVKEIAK-----PNEIMLVVDSMTGQDAVNVAESFDDQLDVTGVTLTKLDGDTRGGAAL 261
88 GGENTSINMSNKPPTVVMMVGLQGAGKTTTAGKLALLMRKKYNKKPMLVAADIYRPAAIN 147
                                                                                                                                                                                     :|| :| :| :| :| :| 339 AIREELNIPVKLIGFGEKIDDIGEFNSENFMKGLL 273
                                                                                                                                                                      SIRSVTQKPIKFVGMSEKLDGLELFHPERMASRIL 296
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1 MAPEGLSERLQATMQKMRGK......GKKGKRNQMQNMLKGMNLPF 455
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1: \cgn2_6/ptodata_2/pubpaa_UUSOB_NEW_PUB.pep:*

2: \cgn2_6/ptodata_2/pubpaa_VUSOB_NEW_PUB.pep:*

3: \cgn2_6/ptodata_2/pubpaa_VUSO6_NEW_PUB.pep:*

4: \cgn2_6/ptodata_2/pubpaa_UUSO6_PUBCOMB.pep:*

5: \cgn2_6/ptodata_2/pubpaa_UUSO7_NEW_PUB.pep:*

6: \cgn2_6/ptodata_2/pubpaa_VUSO7_NEW_PUB.pep:*

7: \cgn2_6/ptodata_2/pubpaa_VUSO7_PUBCOMB.pep:*

7: \cgn2_6/ptodata_2/pubpaa_VUSO7_PUBCOMB.pep:*

9: \cgn2_6/ptodata_2/pubpaa_VUSO9_NEW_PUB.pep:*

10: \cgn2_6/ptodata_2/pubpaa_VUSO9_NEW_PUB.pep:*

11: \cgn2_6/ptodata_2/pubpaa_VUSO9_NEW_PUB.pep:*

11: \cgn2_6/ptodata_2/pubpaa_VUSO9_PUBCOMB.pep:*

12: \cgn2_6/ptodata_2/pubpaa_VUSO9_PUBCOMB.pep:*

13: \cgn2_6/ptodata_2/pubpaa_VUSO9_PUBCOMB.pep:*

14: \cgn2_6/ptodata_2/pubpaa_VUSO0_PUBCOMB.pep:*

14: \cgn2_6/ptodata_2/pubpaa_VUSO0_NEW_PUB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                156504 seqs, 31069816 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 13066, A	Sequence 5420, Ap	Sequence 12128, A	Sequence 4945, Ap	Sequence 10861, A	Sequence 13254, A	Sequence 13525, A	Sequence 2, Appli	Sequence 5755, Ap	Sequence 10263, A	Sequence 11948, A	Sequence 10965, A		Sequence 11562, A	Sequence 10378, A	Sequence 12126, A	5299,		Sequence 11781, A
	ID	US-09-815-242-13066	US-09-815-242-5420	US-09-815-242-12128	US-09-815-242-4945	US-09-815-242-10861	US-09-815-242-13254	US-09-815-242-13525	US-09-814-041A-2	US-09-738-626-5755	US-09-815-242-10263	US-09-815-242-11948	US-09-815-242-10965	US-09-815-242-14089	US-09-815-242-11562	US-09-815-242-10378	US-09-815-242-12126	US-09-815-242-5299	US-09-815-242-10904	US-09-815-242-11781
	DB	10	10	10	10	10	10	10	10	σ	10	10	10	10	10	10	10	10	10	10
	Query Match Length DB	455	455	455	472	477	523	466	523	547	453	457	462	501	448	497	416	316	442	455
о́ю	Query Match	99.4	98.3	98,3	62.4	62.4	57,5				51.2		50.0	49.6	37.6	19.0	18.4	18.3	17.8	17.8
	Score	2261	2235	2235	1418.5	1418.5	1307	1306	1297	1168	1164.5	1150	1138	1127.5	854	432	418	416	404.5	404
	Result No.	1	7	ĸ	4	5	Q	7	ω	σ	10	11	12	13	14	15	16	17	18	19

Score 2261; DB 10; Length 455; Pred. No. 1.3e-154;

99.4%; 99.3%;

Query Match Best Local Similarity

; ORGANISM: Staphylococcus aureus US-09-815-242-13066

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120
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                                                  Length 455;
                                                                                      Indels
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APPLICANI: ASKING, Judith W.
APPLICANI: 2yskind, Judith W.
APPLICANI: Wall, Danial
APPLICANI: Wall, Danial
APPLICANI: Trawick, John D.
APPLICANI: Trawick, John D.
APPLICANI: Tramamoto, Robert T.
APPLICANI: Yamamoto, Robert T.
APPLICANI: Yamamoto, Robert T.
APPLICANI: Yau, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/20/48
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/203,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-12-22
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                                              98.3%; Score 2235; DB 10;
ilarity 98.2%; Pred. No. 9.3e-153;
Conservative 3; Mismatches 5;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020061569A1
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                                                              Best Local Similarity
Matches 447; Conserv
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US-09-815-242-12128
        US-09-815-242-5420
                                              Query Match
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      Indels
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APPLICANT: Yau, H. Howard
ITILE OF INVENTION: Identification of Essential Genes in
TTLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-21
PRIOR PRILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-01-05-38
PRIOR PILING DATE: 2000-01-05-38
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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    Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2001-02-16
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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APPLICANT: Haselbeck, Robert
Matches 452; Conservative
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US-09-815-242-5420
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LENGTH: 455
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                                                                                                                                                                                                          Query Match 62.4%; Score 1418.5; DB 10; Lengt
Best Local Similarity 59.0%; Pred. No. 3e-94;
Matches 273; Conservative 86; Mismatches 89; Indels
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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  PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 4945
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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Patent No. US20020061569A1
                                                                                                                                                   ORGANISM: Enterococcus faecalis
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Zyskind, Judith W.
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Trawick, John D.
Carr, Grant J.
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                                                                                                                                                                     Gaps
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                                                                                                                           Length 455;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/104,078
PRIOR PLILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-24
PRIOR PRILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
                                                                                                                                                                   Indels
                                                                                                                         98.3%; Score 2235; DB 10;
llarity 98.2%; Pred. No. 9.3e-153;
Conservative 3; Mismatches 5;
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                               ORGANISM: Staphylococcus aureus
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                                                             Best Local Similarity
Matches 447; Conserv
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                                                                                  US-09-815-242-12128
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SEQ ID NO 12128
LENGTH: 455
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APPLICANT:
APPLICANT:
                                             TYPE: PRT
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TITLE OF INVENTION: identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                          ; Score 1307; DB 10;
; Pred. No. 3.3e-86;
90; Mismatches 102;
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                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13254
LENGTH: 523
      PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-37
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PRIOR DATE: 2000-12-22
PRIOR PRIOR DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13525, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                           ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                          57.5%;
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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-815-242-13525
                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM:
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                                                                                                                                                                                                                                                                         62.4%; Score 1418.5; DB 10; Length 477; 59.0%; Pred. No. 3e-94; ive 86; Mismatches 89; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                  89; Indels
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-16
PRIOR PLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 10861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13254, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Travick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Tramamoto, Robert T.
                                                                                                                                                                                                                ; ORGANISM: Enterococcus faecalis US-09-815-242-10861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                  Matches 273; Conservative
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Best Local
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LALLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHA 180
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                                                                                                       1 MAFEGLSERLQATMQKMRGKGKLTEADIKIMMREVRLALFEADVNFKVVKEFIKTVSERA
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61 LGSDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTAGK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDFLEQLDQVKNLGPLDDIMKMIPGMNKM 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 KGLDKINMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMKQF
                                                                                                                                                                                                                                                  Length 523;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                    57.0%; Score 1297; DB 10; 54.7%; Pred. No. 1.7e-85;
                                                                                                                                                                                                                                                                                             91; Mismatches 103;
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      CURRENT APPLICATION NUMBER: US/09/814,041A
CURRENT FILING DATE: 2001.03-20
PRIOR APPLICATION NUMBER: 60/191,008
PRIOR PILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FRASESQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 523
          US/09/814,041A
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Publication No. US20020197605a1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SITKO
APPLICANT: ANDO, SITKO
APPLICANT: ATSHI, MKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: TREDA, MASATO
APPLICANT: TREDA, MASATO
APPLICANT: OSCATI, ARIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
                                                                                                                                                                     TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                          Matches 251; Conservative
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Best Local Similarity
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Patent No. US20020103104A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FECTEAU, DOUGLAS A.
APPLICANT: LI, HU
APPLICANT: LI, HU
APPLICANT: STEEL, ANGELA
APPLICANT: STEEL, ANGELA
APPLICANT: WANG, LEI
APPLICANT: WANG, LEI
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APPLICANT: AND POLYPEPTIDES COMPOUNDS MODULATING THEIR ACTIVITY
FILE REFERENCE: GM50069
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54.9%; Pred. No. 3.4e-86;
ive 91; Mismatches 102;
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-21
PRIOR PRING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 13225
SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13525
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.99
Matches 252; Conservative
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APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
      FILING DATE: 2000-05-26
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W
                                                                                                                                                                                                                                                                          ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.0
Matches 231; Conservative
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US-09-815-242-11948
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                       Score 1168; DB 9;
Pred. No. 3.2e-76;
                                                                                                                                                                                                                                                                                                                                                                                                         123 LLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVY---
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CURRENT APPLICATION NUMBER: US/09/815,242
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                               ) ORGANISM: Corynebacterium glutamicum
US-09-738-626-5755
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELIANG DATE: 2000-05-29
PRIOR FILING DATE: 2000-05-29
PRIOR FILING DATE: 5000-05-39
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                     51.4%;
49.1%;
PRIOR FILING DATE: 2000-08-03
                NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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US-09-815-242-10263
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LENGTH: 547
                                                                                              TYPE: PRT
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Best Local
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63 SDVMQSLTPGQQVIKIVQDELTKLMGGENTSINMSNKPPTVVMMVGLQGAGKTTTACKLA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.2%; Score 1164.5; DB 10; Lengt 51.0%; Pred. No. 4.4e-76; live 94; Mismatches 121; Indels
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10263
LENGTH: 453
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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183 EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD 242
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                     CURRENT APPLICATION NUMBER: 05/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/200,848
PRIOR APPLICATION NUMBER: 60/200,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-7
PRIOR PLING DATE: 2000-11-7
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PRIOR PLING DATE: 2000-12-22
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PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-22
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Haemophilus influenzae
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
            FILE REFERENCE: ELITRA.011A
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Matches 225; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 KMKGLDKLNMSEKQIDHIKAIIQSMTPAERNNPDTLNVSRKKRIAKGSGRSLQEVNRLMK 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EHIDFVIIDTAGRIHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 457;
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                     50.6%; Score 1150; DB 10; 50.5%; Pred. No. 4.9e-75; tive 93; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 QFNDMKKMMKQFTGGGKGKKKKKRNQMQNMLKGMNLPF 455
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                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11948
LENGTH: 457
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 5000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2001-02-22
PRIOR PLILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10965, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11948
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Zyskind, Judith W.
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 50.5
Matches 231; Conservative
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US20020061569A1
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Best Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 LLMRKKYNKKPMLVAADIYRPAAINQLQTVGKQIDIPVYSEGDQVKPQQIVTNALKHAKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHLDFVIIDTAGRLHIDEALMNELKEVKEIAKPNEIMLVVDSMTGQDAVNVAESFDDQLD 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.6%; Score 1127.5; DB 10; Length 501;
49.7%; Pred. No. 2.3e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91; Mismatches 130; Indels
                  APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                          CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-10-23
PRIOR PLICATION NUMBER: 60/24,578
PRIOR PLICATION NUMBER: 60/25,625
PRIOR PLICATION NUMBER: 60/25,625
PRIOR PLICATION NUMBER: 60/25,625
PRIOR PLICATION NUMBER: 60/25,931
PRIOR PLICATION NUMBER: 60/25,931
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14089
LENGTH: 501
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CTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-14089
Yamamoto, Robert T.
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Best Local Similarity 49.78
Matches 225; Conservative
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ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
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US-09-815-242-11562
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60 ALGSDVMQSLTPGQQVIKIVQDELTKIMGGENTS-INMSNKPPTVVMMVGLQGAGKTTTA 118
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                                                                                                                                                                                                          APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.6%; Score 854; DB 10; ]
ilarity 39.5%; Pred. No. 7.6e-54;
Conservative 101; Mismatches 153;
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                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
SOFTWARE FaatSEQ for Windows Version 4.0
SEQ ID NO 11562
LENGTH: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                      APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Helicobacter pylori
US-09-815-242-11562
                                                    Ohlsen, Kari L.
Zyskind, Judith W.
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                            APPLICANT: IndexLet, NO.221.

APPLICANT: Olisen, Kari L.

APPLICANT: APPLICANT: Aralid, Judith W.

APPLICANT: Rall, Daviel.

APPLICANT: Grant J.

APPLICANT: Carr, Grant J.

APPLICANT: Carr, Grant J.

APPLICANT: Tamanoto, Robert T.

APPLICANT: Tamanoto, Robert T.

APPLICANT: APPLICANTON: IndexLification of Essential Genes in TILE OF INVENTION: Prokaryotes

FILE OF INVENTION: Prokaryotes

FILE OF INVENTION: Prokaryotes

FILE OF INVENTION: Prokaryotes

FILE APPLICATION NUMBER: 60/121,078

FRIOR PILING DATE: 2000-03-21

FRIOR PELING DATE: 2000-05-25

FRIOR FILING DATE: 2000-05-25

FRIOR FILING DATE: 2000-10-23

FRIOR FILING DATE: 2000-11-27

FRIOR PELING DATE: 2000-11-27

FRIOR PILING DATE: 2000-11-27

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                                                                    Sequence 10378, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Escherichia coli
US-09-815-242-10378
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RESULT 15
US-09-815-242-10378
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